

STIC Search Repor Biotech-Chem Library

STIC Database Tracking Number: 98347

To:

Daniel Sullivan

Location: CM1-11E12

Art Unit:

1636

Thursday, July 17, 2003

Case Serial Number: 09/914191

From:

Beverly Shears

Location: Biotech-Chem Library

CM1-1E05

Phone:

308-4994

beverly.shears@uspto.gov

Search Notes

Daniel,

Due to seq. length, unable to search amino acid query. I did, however, search Seq. ID 1 in the AA dBs.

Beverly

Note: Qy his and 1 Seg 00 99.8% - 100% match



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STIC-Biotech/ChemLib

From: Sent:

Sullivan, Daniel

To:

Tuesday, July 08, 2003 4:18 PM STIC-Biotech/ChemLib

Subject:

Search Request 09914191

Please search for the following in the commercial and issued patent databases:

-a nucleic acid comprising SEQ ID NO:1

Also, I have reason to believe that the reverse complement of SEQ ID NO:1 encodes all or a portion of the following amino acid sequence:

MTHVASQFASSYVFYWRDYFEDQPLLYPPGFDGRVVVYPSNQTLKDYLSWRQADCHINNLYNTVFW ALIQQSGLTPVQAQGRLQGTLAADKNEILFSEFNINYNNELPMYRKGTVLIWOKVDEVMTKEIKLPTE MEGKKMAVTRTRTKPVPLHCDIIGDAFWKEHPEILDEDS

would it be possible to search this amino acid sequence against the commercial and issued patent databases as well?

Thanks, Dan

Daniel M. Sullivan Examiner AU 1636 Room: 12D12 Mail Box: 11E12 Tel: 703-305-4448

Searcher:	_
Phone:	
Location:	
Date Picked Up:	
Searcher Prep/Review:	
Clerical:	
Online time:	

TYPE OF SEARCH:	
NA Sequences:	
AA Sequences:	
Structures:	
Bibliographic:	
Litigation:	
Full text:	
Patent Family:	
Other:	

ENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
ORLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

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U.S. DEPARTMENT OF COMMERCE

SEARCH REQUEST FORM

Requestor's	. same	Serial
Name:	· · · · · · · · · · · · · · · · · · ·	Number:
Date:	Phone:	Art Unit:

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevent citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevent claim(s).

STAFF USE ONLY

Date completed: 07-16-03		Search	Site vendo	IS Comment
Searcher: Bovery 64994		. <u> </u>	STIC	_ IG
Terminal time: 20		<u>-, 376 7</u>	CM-1	STN
Elapsed time:		<u>. 100</u>	Pre-S	Dialog
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PTO-1590 (9-90)

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SUMMARIES

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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                  Copyright
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- protein search, using frame_plus_n2p model OM nucleic Run on:

9, 2003, 12:44:53 ; Search time 38.5 Seconds (without alignments) 4139.422 Million cell updates/sec July

US-09-914-191-1 1096 Title: Perfect score:

598

1 ttggaatagttcttgcttta......ggtgttagtccagattgttg Scoring table: Sequence:

7.0 Xgapext Ygapext Fgapext 6.0 , Delext BLOSUM62 Xgapop 10.0 , X Ygapop 10.0 , Y Fgapop 6.0 , F Delop 6.0 , D 908470 seqs, 133250620 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL-frame+ 12p.model -DEV=xlp
-Q=/Cap2.1/1929FO 5900-1/050914191/runat 09072003 112348 12858/app_query.fasta_1.775
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-Q=/Cap2.1/192FO 5900-1/0509914191 -BND=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORES=DCC -THR MMA=100 -THR MIN-6 -ALIGNS=15
-LIST=45 -DOCALIGN=200 -THR SCORES=EDCC -THR MMA=0 -ALIGNS=15
-USER=US09914191 @CGN 1 1.114 @runat 09072003 112348 12858 -NCPU=6 -ICPU=3
-NO MAAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DBV TIMEDUT=120 -WARN TIMEOUT=30 -THREDS=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database

/gcgdata/geneseq/geneseqp-embl/AA1980.DAT: /slDS2/gcgdata/geneseq/geneseqp-embl/A11982.DAT:/SlDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:/SlDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:/SlDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:/SlDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:/SlDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:/SlDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:/SlDS2/gcgdata/geneseq /geneseqp-embl/AA1989.DAT geneseqp-embl/AA1987.DAT: geneseqp-embl/AA1988.DAT: 'geneseqp-emb1/AA1996. 'AA1993. /AA1995. /AA1991 (SIDS2/gcgdata/geneseg/genesegp-embl/AA1981. (SIDS2/gcgdata/geneseg/genesegp-embl/AA1982. (SIDS2/gcgdata/geneseg/genesegp-embl/AA1983. /geneseqp-embl/ /genesedp-embl/ genesedb-emp] geneseqp-embl /geneseqp-embl genesedb-empl genesedp-embl /SIDSZ/gcgdata/geneseq/gr SIDSZ/gcgdata/geneseq/gr SIDSZ/gcgdata/geneseq/gr SIDSZ/gcgdata/geneseq/gr SIDSZ/gcgdata/geneseq/gr SIDSZ/gcgdata/geneseq/gr SIDSZ/gcgdata/geneseq/gr /SIDS2/gcgdata/geneseg/ /SIDS2/gcgdata/geneseg/ 'SIDS2/gcgdata/geneseg/ /SIDS2/gcgdata/geneseg/

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ALIGNMENTS

AAB94556 standard; Protein; 173 AA (first entry) 26-JUN-2001 AAB94556; RESULT 1 AAB94556

Human protein sequence SEQ ID NO:15324.

Human; primer; detection; diagnosis; antisense therapy; gene therapy

Homo sapiens

EP1074617-A2.

07-FEB-2001.

28-JUL-2000; 2000EP-0116126.

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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypucleotide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's Parkinson's disease, Huntington's diseases, anchortopic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and
assays for receptor activity, arthritis and inflammation, leuraemias where C.N.S disorders.
Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                          Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral scleroslis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acids and polypeptides, useful for treating disorders
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu C, Asundi V, Chen R, Ma Y,
Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; SEQ ID NO 1956; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              such as central nervous system injuries
                                                                                                                                                                                AAM38811 standard; Protein; 298 AA.
                                                                                                                                                                                                                                                                                                     Human polypeptide SEQ ID NO 1956.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JAN-2000, 2000US-0488725.
25-APR-2000, 2000US-0552117.
9-JUL-2000, 2000US-0598042.
19-JUL-2000, 2000US-062312.
03-AUG-2000, 2000US-0653450.
14-SEP-2000, 2000US-0662191.
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                                                                                                                                                                                                                                                                (first entry)
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                                                                298 GATGAAGACAGC
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Wang J, W
Zhao QA,
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(ull-length cDNAs defined in the specification. Where a primer set

comparises: (a) an oligo-dT primer and an oligonucleotide complementary

to the complementary strand of a polynucleotide which comprises one of

congonucleotide comprises at least 15 nucleotides; or (b) a combination

oligonucleotide comprises a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

sequence and an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

sequence and an oligonucleotide comprising a sequence complementary to a

polynucleotide which comprises a 1'-end sequence, where the

oligonucleotide which comprises at least 15 nucleotides and the combination of

the specification. The primer sets can be used in antisense therapy and

in gene therapy. The primers are useful for synthesising polynucleotides,

particularly full-length cDNAs. The primers are also useful for the

connection and/or diagnosis of the abnormality of the proteins encoded by

the full-length cDNAs. The primers allow obtaining of the full-length

cDNAs easily without any specialised methods. AAH0316c to AAH13628 and

AAH13613 to AAH13621 to AAH13632

represent oligonucleotides, all of which are used in the exemplification

of the complementary in the primers and and and and and an antisonal and and an antisonal and an antisonal and antisonal and antisonal and an antisonal and an antisonal and an antisonal and an antisonal and antisonal and an antisonal and antisona
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, Otsuki T;
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Matches:
Conservative:
Mismatches:
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                    99JP-0248036.
99JP-0300253.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                            11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
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Ren F, W Zhang J;

8; SEQ ID 13475; 2537pp + CD ROM; English.

Claim

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                                                                                                 CAACAATCTGGACTAACACCAGTACAAGCCCAAGGGAGATTACAGGGAACTCTTNCAGCA
                                                                                                           GlnGlnSerGlyLeuThrProValGlnAlaGlnGlyAkgLeuGlnGlyThrLeuAlaAla
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                                                                                                                                                  AspLysAsnGlulleLeuPheSerGluPheAsnIleAsnTyrAsnAsnGluLeuProMet
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544.00
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                         Percent Similarity:
Best Local Similarity:
Query Match:
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11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Alignment Scores:
Pred. No.:
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Ishii S,
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The present invention describes primer sets for synthesising 5602

full-length cDNAs defined in the specification. Where a primer set
compirates: (a) an oligo-dT primer and an oligouncleotide compises one of
the complementary strand of a polymucleotide which comprises one of
the 5602 mucleotide sequences defined in the specification, where the
cligonucleotide comprises at least 15 mucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polymucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a polymucleotide which comprises a 5'-end
sequence and an oligonucleotide comprises a 3'-end sequence complementary to a
polymucleotide which comprises a 1'-end sequence of in
the specification. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesising polymucleotides,
particularly full-length cDNAs. The primers are also useful for the
cetection and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers are also useful for the
cDNAs easily without any specialised methods. AAH13628 and
AAH13613 to AAH13621 co AAH13629 to AAH13632
represent thuman amino acid sequences; and AAH13629 to AAH13632
represent constants.
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Matches:
Conservative:
Mismatches:
Indels:
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537.00
98.08%
98.08%
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                                                                                                                                                                                                                                                                                                                                                                                                 the present invention.
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Best Local Similarity:
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DB:
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WPI; 2001-442253/47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                 22-OCT-2001
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Pred. No.:
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                                                                                                                                                                                                                                                                 leukaemia.
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Wang J, V
Zhao QA,
                                                                                                      AAM40597;
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                                                                                                                                                             Нишап
                                                            AAM40597
                                             RESULT
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                                                                                                      Cancer-associated nucleic acid molecules (N) and proteins (P), where cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens. The colon cancer antigens are collectively and cancer antigens. The colon cancer antigens are collectively and cancer antigens. The colon cancer antigens and vector of diseases associated with inappropriate P catagnosis and treatment of diseases associated with inappropriate P cargonistion. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing in a patient's genome that affect the activity of P by expressing in a patient's genome that affect the activity of P by expressing to express the proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and ABB7789 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCAGACAAGAATGAGATTTTGTTTTCTGAATTCAACATCAACTATAATAATGAGCTGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                       Claim 11; Page 6911-6912; 9803pp; English
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                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                               99US-0157137.
                                                                                                    28-SEP-2000; 2000WO-US26524
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100.00%
100.00%
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N-PSDB; AAH33902.
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Best Local Similarity:
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                                           WO200122920-A2.
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                Homo sapiens
                                                                                                                                 29-SEP-1999;
                                                                                                                                              03-NOV-1999;
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DB:
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the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Auntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and threapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                       Human, nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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Zhang J;
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Yang Y,
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Xu C, Xue AJ,
R, Drmanac RT;
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Matches:
AAM40597 standard; Protein; 297 AA
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Wang Z, Wehrman T, X
Zhou P, Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552117.
09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-0653450.
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427.00
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19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGCCAACAGAAATGGAAGGAAAAAAATGGCAGTGACCCGGACCAGGACAAAGCCAGTG 356
                                                                                            The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
 capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAATCTGGACTAACACCCAAGCCCAAGGGAGATTACAGGGAACTCTTNCAGCAGAC
                                                                                                                                                                                                                                                                                                                                                                                          AGGAAAGGGACTGTGTTGATATGGCAGAAGGTGGATGAAGTGATGACAAAAGAAATTAAG
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-------lleLeuGlyGluLy8------SerArgGlnAlaValVal
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47
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Matches:
Conservative:
Mismatches:
Indels:
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99US-0123180.
99US-0123548.
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11-JUL-2000; 2000US-0614150.
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  termination sequence.
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   535 AAGAATGAGATTTTGTTTTCTGAATTCAACATCAACTATAATAATGAGCTGCCGATGTAT 476
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04-AUG-1999
  220 PheValHisSerGluAsnIleAlaGlyArgSerPheTrpAsnGluGlnProSerLeuTyr 239
                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 48411.
                                                    AAG39159 standard; Protein; 520 AA.
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01-APR-1999
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595 CAATCTGGACTAACACCAGTACAAGCCCAAGGGAGATTACAGGGAACTCTTNCAGCAGAC 536
                            355 CCCTTGCACTGCGAT---ATCATCGGGGATGCTTTCTGGAAGGAACATCCAGAGATTCTA 299
                                                                                                                                                                                                                                                                                              238 PheValHisSerGluAsnIleAlaGlyArgSerPheTrpAsnGluGlnProSerbeuTyr 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                 535 AAGAATGAGATTTTGTTTTCTGAATTCAACATCAACTATAATAATGAGCTGCCGATGTAT
                                                                                                                                                             |||:::|||:::
206 ArgGlnGlySerCysLeuPheLysLysValGluGluThrVal-------
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99US-0123180.
99US-012348.
99US-012624.
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990S - 0148684 - 990S - 0149684 - 990S - 0149175 - 990S - 0149175 - 990S - 0149172 - 990S - 0149172 - 990S - 014992 - 990S - 014992 - 990S - 014992 - 990S - 014993 - 990S - 015993 - 990S - 015993 - 990S - 015193 - 990S - 015995 - 990S - 015996 - 990S - 015996 - 990S - 015998 - 990S - 
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27-AUG-1999;
27-AUG-1999;
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-SD66	-S066	-Sn66	-SU66	-S066	-S066	-SU66	- 2066	-S066	-Sn66	-S066	-S066	2000	-SD66	-S066	-Sn66	-5066	-S066	-S066	-S066	-Sn66	-2066	-S066	-S066	-S066	-SU66	9000	-Sn66	99US-)-SD66	- SD66	-Sn66	-Sn66	9908-	-S066	-S066	99US-	-S066	99US-)-S066	99118-)-SD66)-SN66)-Sn66)-S066	-Sn66	99US-(9908-)-SD66)-Sn66	9908-()-S066	99US-)-SN66
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28-APR-1999;
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04-MAY-1999;
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   595 CAATCTGGACTAACACCAGTACAAGCCCAAGGGAGATTACAGGGAACTCTTNCAGCAGAC 536
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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 99US-0161369.
99US-0161360.
99US-0161361.
99US-0161920.
99US-0161993.
99US-0162142.
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99US-0123180.
99US-0125788.
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99US-0129845.
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128.00
56.57%
32.32%
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                                                                                    Percent Similarity:
Best Local Similarity:
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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05-MAR-1999;
09-MAR-1999;
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5-APR-1999;
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21-APR-1999;
23-APR-1999;
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595 CAATCTGGACTAACACCAGTACAAGCCCAAGGGAGATTACAGGGAACTCTTNCAGCAGAC 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   484 ValAspTyrSerAsnIleIleAspGlnCysPheTrpGlnGlnHisProHisIleLeu 502
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Matches:
Conservative:
Mismatches:
Indels:
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128.00
56.57%
32.32%
              99US-0160767
                           99US-0160768
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99US-0160981
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99US-0162142
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Best Local Similarity:
Query Match:
                                   21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
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26-OCT-1999;
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99US-0145192.
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99US-01474303
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99US-01481319
99US-0148341,
99US-0148565
99US-0148565
99US-0149368
99US-0149722,
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99US-0149930
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99US-0155139
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99US-0155486
99US-0156458
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99US-0157753
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99US-0145086
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99US-0159331.
99US-0159637.
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RR 25-FEB-1999 9918-0121825.
RR 27-WR-1999 9918-0121826.
RR 29-WR-1999 9918-0122180.
RR 29-WR-1999 9918-0122180.
RR 10-ARR-1999 9918-0122180.
RR 11-ARR-1999 9918-012222.
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PR 12-JUL-1999; 99US-0142377.

PR 13-JUL-1999; 99US-0144065.

PR 15-JUL-1999; 99US-0144065.

PR 16-JUL-1999; 99US-0144085.

PR 16-JUL-1999; 99US-0144086.

PR 19-JUL-1999; 99US-0144332.

PR 19-JUL-1999; 99US-0144332.

PR 19-JUL-1999; 99US-0144332.

PR 20-JUL-1999; 99US-0144332.

PR 20-JUL-1999; 99US-0144333.

PR 20-JUL-1999; 99US-0144333.

PR 20-JUL-1999; 99US-0144332.

PR 20-JUL-1999; 99US-0144332.

PR 20-JUL-1999; 99US-0144332.

PR 22-JUL-1999; 99US-0144332.

PR 23-JUL-1999; 99US-0144331.

PR 23-JUL-1999; 99US-0145218.

PR 24-JUL-1999; 99US-0145319.

PR 25-JUL-1999; 99US-0145319.

PR 25-JUL-1999; 99US-0145319.

PR 25-JUL-1999; 99US-0145319.

PR 25-JUL-1999; 99US-014336.

PR 25-JUL-1999; 99US-0149378.

PR 25-JUL-1

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ProSerThrProThrProProProArg------ 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValGlySerLeuSerProProProProAlaSerPro-SerGlyGlyArgSerProSerTh 206
                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an B-value sequences are actor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTTCCTTCCCTGTTCCCCTCCCAACTTGAGTTGTCTCATTCGCACCAGTGTCCTGGGTG 193
                                                                                                                                                                                                                                                                                            Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGAGGCCTTGCATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254 TAAGCACACAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTAGAATCTCTGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGGCACTGGCTTTGTCCTGGT
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                                                                                                                                                                                                                                                                                                                                                                    Claim 5; SEQ ID NO 1632; 261pp + Sequence Listing; English
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93
46
20
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Conservative:
Mismatches:
Indels:
           Herbicidally active polypeptide SEQ ID NO 1632.
                                       Herbicidal, plant, agriculture, herbicide
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38.89%
30.56%
8.26%
                                                                                                                                                                                                                                     Tietjen K, Weidler M;
                                                                  Arabidopsis thaliana
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Best Local Similarity:
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                                                                                              WO200210210-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGCCAACAGAAATGGAAGGAAAAAAGATGGCAGTGACCCGGACCAGGACAAAGCCAGTG 356
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LysAsnGluLeuLeuSerGlnGlnPheGlyIleGluTyrAsnSerLeuProValIlePhe
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334
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Matches:
Conservative:
Mismatches:
Indels:
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                                   990S - 0157865
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128.00
56.57%
32.32%
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Best Local Similarity:
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990S-0146389.
990S-0147038.
990S-0147204.
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99US-0140353.
99US-0140354.
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99US-0140991.
99US-0141287.
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99US-0145192.
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99US-0147260
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99US-0145919
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99US-0146386
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                                                                                                             Protein identification, signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 75712.
                               AAG58628 standard; Protein; 128 AA
                                                                                                                                                                                                                                    99US-0121825.
99US-0123180.
99US-0123180.
99US-0125788.
99US-0126785.
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99US-0126786.
99US-0126786.
99US-01308714.
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99US-013186.
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99US-0138540.
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99US-0139119.
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99US-0137528.
99US-0137502.
99US-0137724.
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99US-0139456.
99US-0139457.
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                                                                    18-OCT-2000 (first entry)
                                                                                                                                                      Arabidopsis thaliana
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                                                                                                                                                                                               06-SEP-2000
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                                                  AAG58628;
         RESULT 14
AAG58628
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193 GGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGAGGGCCTTGCATGG 252
                                                                               253 TTAAGCACACCAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTAGAATCTCTGGAT 312
                                                                                                                              313 GTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGGCAAAGGGCA---CTGGCTTTGTCC 369
                                                                                                                                                                                                                                                                                                                                    Zebrafish, differentiation enhancing factor, ankyrin repeat, C2 domain, SH3 consensus binding sequence; pleckstrin homology domain; adipogenesis; neurogenesis; hyperplastic disease; neoplastic disease; nervous system.
49
                                                                                             69 ArgProGluLysLysGlnSerAspLysSerAsnTyrAlaArgAlaGluLeuPheArgGly 88
                                                         ----LeuLeuTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used
for
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neurogenesis, e.g.
                                                                                                                                                                                                                                                                                                                Zebrafish differentiation enhancing factor 2 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding differentiation
particularly to regulate adipogenesis and
treating tumours and neurological disease
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                                                                                                                                                                                                                                            AAW77288 standard; Protein; 982 AA.
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                                                                                                                                                                          370 TGGTCCGGGTCACTG 384
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                                                                                                                                                                                                                                                                                         (first entry)
                                                         SerArgGlnThr---
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Thomas RM;
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Mismatches:
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                                                       99US-0150884.
99US-0151065.
99US-0151066.
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99US-0156458.
99US-0156596.
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99US-0160768.
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99US-0161992.
99US-0161993.
99US-0162142.
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99US-0157753.
99US-0157865.
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99US-0154018
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99US-0159293
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31.43%
8.07%
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Best Local Similarity:
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                                                                     27-AUG-1999
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27-AUG-1999
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                                             25-AUG-1999
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The differentiation enhancing factors (DEF), comprise at least one each of SH3 consensus binding sequence, ankytin repeat, pleckstrin homology domain and C2 domain. The DEF induce adipogenesis or neurogenesis; they are mediators of SH3-domain dependent signalling and may be involved in cellular gene expression, cytoskeletal architecture, protein trafficking, endocytosis or adhesion, migration, proliferation and differentiation of calls. Typical applications of DEF and agents that modulate interaction between the protein and it's ligand, or of nucleic acid expressing them, are treatment of hyperplastic and neoplastic disease (a wide range of solid tumours and leukaemias), including metastases; for in vitro induction of differentiation of neural creat calls to neurons, glial cells etc.; for increasing neuron survival, and inducing cell creat, in the nervous system (e.g. treatment of traumatic injury, stroke, Alzheimer's, Parkinson's or Huntington's diseases, amylotrophic lateral sclerosis, multiple sclerosis etc.).

85 AACAAGGTGTTCTGCTTAAAC-----AGAGTAAGATACACCACCCCCATCCAT 132

US-09-914-191-1 (1-598) x AAG58628 (1-128)

8 셤 ò

133 CCCTTCCTTCCCTGTTCCCCTCCCACTTGAGTTGTGTCATTCGCACCAGTGTCCTGGGT 192 :::|||
3 SerlysalalleCysLeuGlyPheLeuProProArgLeuArgPheSerSerProArgLeu

Sequence 982 AA;

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389 GATGGCAGTGACCCGGACCAGGACAAAGCCAGTGCCCTTGCACTGCGATATCATCGG--- 333
                                                                                                                                                                          ---TCCAGA 306
                                                                                                                                                                                       739 AspGlyArgAspLeuValLysAspLysGlnArgPheValProAsnLeuValAsnAsnGlu 758
                                                                                                                                                                                                                                                                        260 ------GIGCTIAACCAIGCAAGCCCICCCACCICCCAGGGCTCCTIGCCTIAG 213
                                                                                                                                                                                                                                                                                     212 GTGGCTGTAGCATCCCTACCACCAGGACACTGGTGCGAATGACACACTCAAGTTGGGA 153
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          Length:
Matches:
Conservative:
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Indels:
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APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Thomas, Mary Beth
APPLICANT: Portanen, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Mary COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CARL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
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US-08-344-616-32

US-08-344-616-32

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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 389, Application US/09461697; Patent No. 6277974; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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   SEQ ID NO 389
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Query Match:
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-Q=/cgn2_1/USPTO_spool/US09914191/runat_09072003_112350_12911/app_query.fasta_1.775
-D=1ssued Patents AA -QFWT=fastan -SUFFIX=rai -MINNATCH=0.1 -LOOPCL=0
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFWT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US09914191_@CGN_1 128 @runat_09072003_112350_12911 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NGG SCORES - WAT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 375, App
Sequence 10, Appl
Sequence 6, Appli
Sequence 2, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 395, App
Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 9, Appli
                                                                                                                    9, 2003, 12:46:48; Search time 13.5 Seconds (without alignments) 2606.653 Million cell updates/sec
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                    GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                  protein search, using frame_plus_n2p model
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US-09-461-697-375
US-09-66-697-373
US-09-056-285A-10
US-08-097-6
US-08-481-126-3
US-08-481-1481-1481-16
US-09-461-697-395
US-08-461-697-395
US-08-461-697-395
US-09-118-408-8
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
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length: 2000000000
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TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323 GAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTGGCTTTGTCCT
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Conservative:
Mismatches:
Indels:
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APPLICANT: Lo. Donald C.
APPLICANT: Lo. Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Ratz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR;
TITLE OF INVENTION: COMPOSITIONS, DIS,
TITLE OF INVENTION: CELL DEATH
FILE REPERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT APPLICATION NUMBER: US/09/461,697
NUMBER OF SEQ ID NOS: 466
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Patent No. 6403307
GENERAL INFORMATION:
APPLICANT: Stone, Edwin M.
Sheffield, Val C.
                                                                                            Sequence 373, Application US/09461697; Patent No. 6277974; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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US-09-461-697-373
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Pred. No.:
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APPLICANT: Barney. Sharney. Shart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Wasturi
APPLICANT: Wasturi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
                                                                                                                                                         -----TGTTGGCAG 415
                                                                                                                                                                                                                                                           ... TrpArgAsnMetAsnThrlleLysGlyThrGlnAsnTyrlleProAlaLysCysPheSer 167
                                                                             --GGTCCGGGTCACTGCCATCTTTTTCCTTCCAT 403
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                                                                                                                  59 AspSerAspPheCysIlePheAspLeuLysThrGlyPheCysProLeuAsnSerPheGln 78
                                                                                                                                                                                            79 TrpArgAsnMetAsnThrIleLysGlyThrGlnAsnTyrIleProAlaLysCysPheSer 98
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|GluAlaAspArgAspIleMetThrLeuAlaAsnHisTrpAsnCysProValLeuSerSer
    GAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTGGCTTTGTCCT
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                                                                                                                                                                                                                                                                                                                ------CAACACAGTCCCTTTCCTATA 478
                                                                                                                                                                                                                                                                                                                                                     119 ValLeuCysGlyAsnAspHisValAsnLeuProile 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----CAACACAGTCCCTTTCCTATA 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-914-191-1 (1-598) x US-09-461-697-375 (1-488)
                                                                                                                                                                                                                                     CTTAATTTCTTTTGTCATCACTTCATCCAC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTAATTTCTTTTGTCATCACTTCATCCAC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 375 LENGTH: 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                       TTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 375, Application US/09461697
Patent No. 6277974
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.00
33.70%
26.09%
6.93%
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                             1-697-375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM:
                                      39
                                                                           371
                                                                                                                                                                                                                                   416
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738 ArgAlaHisSerThrAlaVal------GlyIlePheSerValLeuValPhe 753
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                                                                                                                                                                                       APPLICANT: Hammond, H. Kirk
APPLICANT: Insel, Paul A.
APPLICANT: Ping, Peipei
APPLICANT: Post, Steven R.
APPLICANT: Post, Steven R.
APPLICANT: Gao, Meihua
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
TITLE OF INVENTION: HEART FAILURE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SUFTWARE: FastSED for Windows Version 2.0
SUFRENT APPLICATION DAY
APPLICATION NUMBER: US/09/008,097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-'09-914-191-1 (1-598) x US-09-008-097-6 (1-1167)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 TCCCTTCCTTCCCTGTTCCCCTCCCAACTTGAG---
                                                                                                                                                                                                                                                                                                                                                                          SEE: MORRISON & FOERSTER
': 755 PAGE MILL ROAD
PALO ALTO
                                                                                                                                     Sequence 6, Application US/09008097; Patent No. 6306830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37,612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                         231 sGlyAlaLeuValrrp 236
                      67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Dylan, Tyler M
REGISTRATION NUMBER: 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1167 amino acids
                      CGGTGTTGGAACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.93%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94304-1018
                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Hammon
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: lin/
MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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STREET: 755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3-09-008-097-6
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                    82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 GlualadinGluGlyLeuGlnGlyGlnLeuGlyAlaLeuArgArgGluArgAspGlnLeu 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       529 GAGATITIGITITICIGAATICAACATCAACTATAATAATGAGCTGCCGATGTATAGGAAA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     469 GGGACTGTGTTGATATGGCAGAAGGTGGATGAGATGACAAAAGAAATTAAGCTGCCA 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||:::
-----AspLysSerAlaLeuGluGluGluLysArgGln 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GTGACC 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 LeuGluGlnGluAsnGluAspLeuAlaArgArgLeuGluSerSerSerGluGluValThr 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           376 CGGACCAGGACAAAGCCAGTGCCCTTGCACTGCGATA---TCATCGGGGATGCTTTCTGG 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319 A---AGGAACATCCAGAGATTCTAGATGAAGACAGCTGACCCTTTTGCGCTTCAGTTCTG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 ySerArgGluValSerGlnTrp-----AsnLeuAspThrLeuAlaPheGln---- 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 GIGTGCTTAACCATGCAAGCCCTCCCACCTCCCAGGGCTCCTTGCCTTAGGTGGCTGTAG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 uValProAlaSerGinIleLeuLysGluAsnProSer-----GlyArgProArgSe 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --Cy 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 GluThrGlnThrArgAspLeuGluAlaAlaTyrAsnAsnLeuLeuArg-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --GluLeuLysSerGluLeuThr----
                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4490
100
100
100
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/056,285A
FILING DATE: 07-Apr-1998
ATTORNEY/AGENT INFORMATION:

NAME: Arnold, Beth E.

REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-010.28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-914-191-1 (1-598) x US-09-056-285A-10 (1-490)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 409 ACAGAAATGGAAGGAAAAAAAGATGGCA-----
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-056-285A-10
                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 490 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 617-832-1000
                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-832-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224 rLysGluGlyAspLysGly
                                                                            COMPUTER READABLE FORM:
                                                       ZIP: 02109-2170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.88%
CITY: Boston
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
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1167 32 22 46 30

Conservative: Mismatches: Indels:

Length: Matches:

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OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,126
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRILING DATE: 08/326,347
FILING DATE: 20-0CT-1994
APPLICATION NUMBER: 08/973,307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARFILING DATE: 09-NOV-1992
FILING DATE: 09-NOV-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   144 MetArgSerLysProProFroGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inch diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08484126
Patent No. 5985655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Anderson, W. French
APPLICANT: Baltrucki, Leon F.
APPLICANT: Mason, James M.
TITLE OF INVENTION: Targetable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carella, Byrne,
Cecchi, Stewart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Lillie, Raymond J
REGISTRATION NUMBER: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 453 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, BADDRESSEE: Cecchi, St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roseland: New Jersey
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                 137 -----
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                                                                                         330 TCCCCGATGATATCG------CAGTGCAAGGGCACTGGCTTTGTCCTGGTCCGG 377
                                 754 ThrSeralaileAlaAsnMetPheThrCys-----AsnHisThrProlleArgSerCys 771
                                                                     378 GTCACTGCCATCTTTTTCCTTCCATTTCTGTTGGCAGCTTAATTTCTTTTGTCATCACT
                                                                                                                                                                                                                                                                                                                                                                              ACTUICANT: Bazan, J. Fernando
APPLICANT: Bazan, J. Fernando
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: PURIFIED MAMMALIAN T CELL ANTIGENS AND
TITLE OF INVENTION: RELATED REAGENTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
STREFT
219 CAAGGAGCCCTGGGAGGTGGAGGGCTTGCATGGTTAAGCACACC
                                                                                                                                                         393
34
116
46
39
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SOFTWARE: Patentin Release #1.0, Version #1.25
STATE APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-914-191-1 (1-598) x US-08-429-742-2 (1-393)
                                                                                                                                                                                                                                                                                                    438 TCATCCACCTTCTGCCATATCAACACAGTC 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: DNAX Research Institute
901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/429,742
FILING DATE: 26-APR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ching, Edwin P.
REGISTRATION UNBER: 34,090
REFERENCE/DOCKET NUMBER: DX0505
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08429742
Patent No. 5686257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-429-742-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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                                                                                                                                                                                                                                                                                                             826
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Query Match:
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---CCAGTACAAGCCCAAGGGAGATTACAGGGA 551

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118 ProPhelysProIle---LeuGluAlaSerVallleArgLysGlnAsnGlyGluGluHis 136
                                                                                                                                                                                                                        93 Glu--------GlyvalTyrLysCysLeuHisTyrSerAspSerValSer 106
                                                                                                                                                                                                                                                                                                     -----ValValLeuMetCysSerThr 143
                                                                         550 ACTCTINCAGCAGACAAGAATGAGATTTTGTTTTCTGAATTCAACATCAACTATAATAAT 491
                                                                                                                                                                        490 GAGCTGCCGATGTATAGGAAAGGGACTGTTGATATGCCAGAAGGTGGATGAAGTGATG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 CCAGAGATTCTAGATGAAGACAGCTGACCCTTTTGCGCTTCAGTTCTGGTGTTTAACC 251
                                                                                                        250 ATGCAAGCCCTCCCACGCGCTCCTTGCCTTAGGTGGCTG 206
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                           : 1012 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                         TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                          single
   COMPUTER READABLE FORM:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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DB:
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                                                                                                                                                                                                                                              155 CCAACTTGAGTTGTGTCATTCGCACCAGTGTCCTGGGTAGGAGGATGCTACAGCCACCT 214
                                                                                                                                                                                                                                                                                                                                                       215 AAGGCAAGGAGCCCTGGGAGGTGGGAGGGCTTGCATGGTTAAGCACACCAGAACTGAAGC 274
                                                                                                                                                                                                                                                                                                                                                                                                                       315 Asp-----LysThrGinGluCysTrpLeuCysLeuValSerGlyProProTyrTyrGlu 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||| :::||| ::: 333 GlyValAlaValLeuGlyThrTyrSerAsnHisThrSerAlaProAlaAsnCysSerVal 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 392 TITICCTICCATITCTGTIGGCAGCTIAATTICTITIGICATCACTICATCCACCTICTG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               353 AlaserGlnHis-----LysLeuThrLeu-SerGluValThrGlyGlnGlyLeuCy 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 452 CCATATCAACACAGTCCCTTTCCTATACATCGGCAGCTCATTATTATAGTTGATGTTGAA 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----LeuCysAs 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               512 ITCAGAAAACAAAATCTCA------TTCTTGTCTGCTGNAAGAGTTCCCTGTAA 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----CCTGGTCCGGGTCACTGCCATCTT 391
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|s---ValGlyAlaValProLysThrHisGlnAla-----
                                                                                                                                                                                                                                                                                                                                                                                       288 ProserGlnGlnProGlyThrGlyAspArgLeuLeuAsn-
                                                                                                              Conservative:
Mismatches:
Indels:
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GENERAL INFORMATION:
APPLICANT: Kindsvogel, Wayne
APPLICANT: Jelinek, Laura J.
APPLICANT: Hagopian, William A.
APPLICANT: Hagopian, William A.
APPLICANT: LaGasse, James M.
TITLE OF INVENTION: ISLET CELL ANTIGEN 1851;
NUMBER OF SEQUENCES: 34
CORRESSEE: ZymoGenetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            560 TCTCCCTTGGCTTGT---ACTGGTGTTAGTCCA 590
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275 ProSerGlyThrValSerMetValProGlyAla----
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                                                                                Length:
Matches:
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COUNTRY: USA
                  xenotropic gp70 protein
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Patent No. 6300093
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33.85%
22.92%
6.61%
                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
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                NAME/KEY:
                                                               Alignment Scores:
                              US-08-484-126-3
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FEATURE:
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189 GGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGAGGCCTTGC 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 ATGGTTAAGCACACCAGAACTGAAGCGCAAAAG------GGTCAGCTGTCTTCATCT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 AGAATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 GlyArgLeuGlyCysLeu----LeuGluGluGlyLeuCysGlyAlaSerGluAlaCys 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 GluValSerProValAlaLeuGlnArgLeuArgValAlaLeuGlnLysLeuSerGlyThr 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 ProAlaAlaProSerSerValPro-------HisGlyArgGlnLeuPro 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Barney, Sham
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Katz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1012
26
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Matches:
Conservative:
Mismatches:
Indels:
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/811,481
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-461-697-395
; Sequence 395, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/ASBYT INFORMATION:
NAME: Lingenfelter, Susan
REGISTRATION NUMBER: P-41,156
REPRENCE/POCKET NUMBER: 95-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6675
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SEQ ID NO 8
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TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-99
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: PSESSEQ for Windows Version 4.0
SEQ ID NO 395
LENGTH: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 IleLysGlyThrGlnAsnTyrIleProAlaLysCysPheSerLeuAspAlaPheCysHis 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetThrieuAlaAsnHisTrpAsnCysProValLeuSerSerAspSerAspPheCysIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 PheAspLeuLysThrGlyPheCysProLeuAsnSerPheGlnTrpArgAsnMetAsnThr 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||||| :::
61 HisPheSerAsnMetAsnLysAlaLeuLeuProLeuPheAlaValLeuCysGlyAsnAsp 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 -----GTTCCGGGTCACTGCCATCTTTTTCCTTCCATTTC-------
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Patent No. 5869330

GENERAL INFORMATION:
APPLICANT: Scherer, Philipp E.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
ADDRESSEB: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                               375
22
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18
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                              341 ATCGCAGTGCAAGGGCACTGGCTTTGTCCT
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REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH195-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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72.00
32.56%
25.58%
6.57%
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STREET: Two ...
CITY. Lexington
The Massachusetts
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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                                                                                                                                                                 TYPE: PRT
CAGANISM: Homo sapiens
US-09-461-697-395
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Pred. No.:
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241 CTCCCACCTCCCAGGGCTCCTTGCCTTAGGTGGCTGTAGCAT---CCCTACCACCAGGA 185
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32 ValProProProLysGlyThrCysAlaGlyTrpMetAlaGlyIleProGlyHisProGly 51
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Patent No. 6197930

GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOWOLOGS
FILE REFERENCE: 97-49

CURRENT APPLICANTON NUMBER: US/09/140,804

CURRENT FILING DATE: 1998-08-26

BARLIER APPLICATION NUMBER: 60/056,983

EARLIER FILING DATE: 1997-08-26

NUMBER OF SEQ ID NOS: 47

SOFTWARE: FastSEQ for Windows Version 3.0
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Matches:
Conservative:
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US-09-118-408-3
Sequence 3, Application US/09118408A
; Patent No. 62565544
; GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEPAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                         : 247 amino acids amino acid
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38.46%
6.43%
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71.00
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ORGANISM: Homo sapiens
                                                                                                                              linear
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Best Local Similarity:
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Best Local Similarity:
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                                                                                           LENGTH:
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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Randall, Douglas D.

APPLICANT: Morency, Brian A.

APPLICANT: Morency, Brian P.

APPLICANT: Morency, Brian P.

TITLE OF INVENTION: BRANCHED CHAIN OXOACID DEHYDROGENASE AND TITLE OF INVENTION: BRANCHED COMPONENTS TO CURRENT PRILING DATE: 1998-06-30

EARLIER APPLICATION NUMBER: 60/051,291

EARLIER FILING DATE: 1997-06-30

EARLIER FILING DATE: 1997-06-30

EARLIER FILING DATE: 1997-06-30

EARLIER FILING DATE: 1998-03-02

NUMBER: 60/076,544

EARLIER FILING DATE: 1998-03-02

NUMBER: 60/076,544
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: P. purpurea
US-09-108-020-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
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 US-09-108-020-43
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US-08-952-981A-2
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32 ValProProDysGlyThrCysAlaGlyTrpMetAlaGlyIleProGlyHisProGly 51
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-----AsnGlyThrProGlyArgAspGlyArgAspGly 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ### Sequence 3, Application US/09506855

| Sequence 3, Application US/09506855 |
| Sequence 3, Application US/09506855 |
| GENERAL INFORMATION: |
| APPLICANT: Sheppard, Paul O. |
| APPLICANT: Lasser, Gerald W. |
| APPLICANT: Lasser, Gerald W. |
| TITLE OF INVENTION: IMMUNE FUNCTION |
| TITLE OF INVENTION: IMMUNE FUNCTION |
| FILE REFERENCE: 99-12 |
| CURRENT APPLICATION |
| WUMBER OF SEQ ID NOS: 50 |
| SOFTWARE: PastSEQ for Windows Version 3.0 |
| SEQ ID NO 3 |
| LENGTH: 247
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-30
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Mismatches:
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Matches:
                                                CURRENT APPLICATION NUMBER: US/09/118,408A CURRENT FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/053,154
EARLIER FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
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; ORGANISM: Homo sapien
US-09-118-408-3
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ORGANISM: Homo sapien
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||||||| 150 ThrProTyrAsnAlaLysGlyLeuLeuLysSerAlaIle---ArgAspAsnAsnProVal 168 ------ACTGTGATAGGAAAGGG-----ACTGTGATA 455 209 TyrSerArgMetArgHisHisValThrGluAlaLeuProLeuLeuLeuAsnAspGlyTyr 228 249 ServalLysLysThrHisArgValLeuIleValGluGluCysMetLysThrAlaGlyIle 268 269 GlyAlaGluLeulleAlaGlnIle-----AsnGluHis-----LeuPheAspGluLeu 284 583 ACACCAGTACAAGCCCAAGGGAGATTACAGGGAACTCTTNCAGCAGACAAGAATGAGATT 524 289 AGCTGACCCTTTTGCGCTTCAGTTCTGGTGTGCTTAACCATGCAAGCCCTCCCACCTCCC 230 349 CACTGCGATATCATCGGGGATGCTTTCTGGAAGGAACATCCAGAGATTCTAGATGAAGAC 523 TIGITITCIGAATICAACAICAACIAIAAI-----AAIGAGCIGCCG 454 TGGCAGAAGGTGGATGAAGTGATGACAAAAGAAATTAAGCTG----333 333 233 252 952

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|1239 GlyProLysThrCysSerAsnThrTrpHisGlyThrPheProlleAsnAlaTyrThrThr 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1183 LysThrTrpLeu------GinSerLysLeuLeuProGlnLeuProGlyValProPhe 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417 ---AGCTGCCAACAGAAATGGAAGGAAAAAAGATGGCAGTGACCCGGACCAGGACAAAGC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 TAGATGAAGACAGCTGAC------CCTTTTGCGCTTCAGTTCTGGTGTGCT 256
                                           APPLICANT: DE FRANCESCO, Raffaele
APPLICANT: TOMEI, Licia
APPLICANT: TOMEI, Licia
APPLICANT: BEHRENS, Sven-Erik
TITLE OF INVENTION: METHOD FOR REPRODUCING IN VITRO THE RNA-DEPENDENT RNA
TITLE OF INVENTION: POLYMERASE AND TERMINAL NUCLEOTIDYL TRANSFERASE
TITLE OF INVENTION: ACTIVITIES ENCODED BY HEPATITIS C VIRUS (HCV)
FILE REFERENCE: IT0002P
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24
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19
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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|1259 GlyProCysThrProSerProAlaPro 1267
                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/08/952,981A
CURRENT FILING DATE: 1998-03-23
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
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Sequence 2, Application US/08952981A
Patent No. 6383768
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: CDNA clone pCD (38-9.4)
US-08-952-981A-2
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70.50
41.57%
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Best Local Similarity:
Query Match:
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LENGTH: 2201
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Search completed: July 9, 2003, 12:51:58 Job time : 19.5 secs

Sequence:

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Searched:

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APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptid
FILE REFERENCE: PAOGSP1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US(US00/26524)
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
                                        Sequence 373, App
Sequence 167, App
Sequence 167, App
Sequence 107, App
Sequence 107, App
Sequence 11, App
Sequence 11, App
Sequence 12, App
Sequence 16, App
Sequence 16, App
Sequence 1331, App
Sequence 395, App
Sequence 383, App
Sequence 383, App
Sequence 383, App
Sequence 37, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 37, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 389, Apr
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Sequence 4, P
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Sequence 2,
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Sequence 12
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0 US-09-815-224-14005

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0 US-09-9176-976-4

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0 US-09-916-849A-3

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0 US-09-116-8425-7

0 US-09-116-843A-3

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US-10-1189-971-14
                                           US-09-922-261-373
US-09-76-240-6
US-09-984-130-144
US-10-184-644-107
US-10-184-644-107
US-10-184-644-107
US-10-184-634-107
US-09-896-738-18
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Matches:
Conservative:
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Percent Similarity:
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LENGTH: 85
   ORGANISM:
    0000000000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Command line parameters:
-MODEL=frame+ n2p.model.-DEV=x1p
-QODEL=frame+ n2p.model.-DEV=x1p
-Q=/Cgn2_1/USFTO_spool/US09914191/runat_09072003_112351_12946/app_query.fasta_1.775
-Q=/Cgn2_1/USFTO_spool/US09914191/runat_09072003_112351_12946/app_query.fasta_1.775
-DB=Published_Applications_AA.-QFMT=fastan.-SUFFIX=rapb.-MINMATCH=0.1
-LOOPCLL=0.-LOOPEXT=0.-UNITS=bits.-STRAT=1.-END=-1.MATRIX=blosum62
-TRANS=human40.cdi.-LIST=45.-DOCALLGN=200.-THR SCORE=pct.-THR MAXEL=0.00
-MAXIEN=2000000000 -USER=US09914191_@CGN 1 1.7 @runat_09072003_112351_12946
-NOFUSE -ICPUS=3.-NO WMAP -LARGEQUERY -NGG_SCORES=0.-WAIT -DSPBLOCK=100
-LONGLOG.-DEV TIMEOUT=120.-WARN TIMEOUT=30.-THREADS=1.*ARAPOP=10.-XGAPEXT=0.5
-FGAPOP=6.-FGAPEXT=7.-YGAPOP=10.-YGAPEXT=0.5.-DELOP=6.-DELOF=6.-DELOF=6.-DELOF=7.
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Sequence 302, App
Sequence 1529, Ap
Sequence 1, Appli
                                                                                                    // Search time 31 Seconds
(without alignments)
4491.550 Million cell updates/sec
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/ cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/NEO7_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                        - protein search, using frame_plus_n2p model
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US-09-934-455-302
US-09-925-300-1529
US-09-844-281-1
                                                                                                                                                                                                                                                                                                                                          of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Ygapop 10.0 , Y
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Match Length
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131 ATCCCTTCCTTCCCTGTTCCCCTCCCAACTTGAGTTGTGTCATTCGCACCAGTGTCCTGG 190
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305 ThrlleLeuProPheTyrProProProAlaTyrTrpSerCysProGlyValSerProGly 324
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                                                                        285 ValproCysPheProGlyProProProThrTrpProTyrAlaTrpAsnGlyValSerTrp
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; Sequence 1529, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Craig Rosen,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies;
FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT APPLICATION NUMBER: DCT/US00/05988
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR PILING DATE: 2001-08-10
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1529
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Matches:
Conservative:
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ORGANISM: Homo sapiens
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Query Match:
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                                                                                                               541 GCAGACAAGAATGAGATTTTTTTTTTTTGAATTCAACATCAACTATAATAATGAGCTGCCG 482
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                                                                                                                                                                                                             21 MetTyrArgLysGlyThrValLeuIleTrpGlnLysValAspGluValMetThrLysGlu 40
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APPLICANT: 10, cuc_aranty
APPLICANT: 10, cuc_aranty
TITLE OF INVENTON: Genes for Modifying Plant Traits IV
FILE REPRENCE: MB1-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: MB1-0022
PRIOR APPLICATION NUMBER: MB1-0022
PRIOR APPLICATION NUMBER: MB1-0023
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
SOFTWARE: PatentIn version 3.1
SEQ ID NO 302
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Keddie, James
Pilgrim, Marsha
Ratcliffe, Oliver
Reuber, Lynne
Riechmann, Jose Luis
Yu, Guo-Liang
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US-09-934-455-302
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APPLICANT: Creelman, Robert
APPLICANT: Dubell, Arnold
APPLICANT: Heard, Jacqueline
   100.00%
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Query Match:
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NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
                         Mary Beth
', Stuart D.
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                                         Portbury, Stuart
Puranam, Kasturi
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ORGANISM: Homo sapiens
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529 rGlyValValAlaGluGlyGlyLeuAspValValThrr---AspSerGlySerIleGl
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Sequence 1, Application US/09844281

Patent No. US2002082386A1

GENERAL INFORMATION:

APPLICANT: Mangold, Beverly L.

APPLICANT: Aldrich, Jennifer L.

APPLICANT: O'Brien, Thomas

TITLE OF INVENTION: Anthrax Specific Antibodies

FILE REFERENCE: 38602.0003

CURRENT APPLICATION NUMBER: US/09/844,281

CURRENT PILING DATE: 2001-04-30

FRIOR FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 3

SOFTWARE PATENTING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn version 3.1
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Mismatches:
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Patent No. US20020111471A1
GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
                                                                                                                                                                                                                                                                                             ; ORGANISM: Bacillus anthracis
US-09-844-281-1
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Pred. No.:
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APPLICANT: Katz, Lawrence C.
TITLE OF INVENTION: AND TERATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL DEATH
FILE REPERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/922,261
CURRENT APPLICATION NUMBER: US/09/461,697
PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING

TITLE OF INVENTION: CAND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING

TITLE OF INVENTION: CELL DEATH
FILE REPRENCE: 10001-005-999

FULLS REPRENCE: 10001-005-999

FURNING PAPLICATION NUMBER: US/09/922,261

PRIOR APPLICATION NUMBER: US/09/461,697
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Matches:
Conservative:
Mismatches:
Indels:
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Patent No. US20020111471A1
GENERAL INFORMATION:
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Thomas, Mary Beth
Portbury, Stuart D.
Puranam, Kasturi
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APPLICANT: KATZ, LAWTENCE C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
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98 GluAlaGlnGluGlyLeuGlnGlyGlnLeuGlyAlaLeuArgArgGluArgAspGlnLeu 117
                                                                                                                                                                                                                             529 GAGATITIGITITCIGAATICAACAICAACIATAATAATGAGCIGCCGATGTATAGGAAA 470
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  Conservative:
Mismatches:
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207 uValProAlaSerGlnIleLeuLysGluAsnProSer-
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2001-08-03
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PRIOR FILING DATE: 1999-12-14
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Patent No. US20020111471A1
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Puranam, Kasturi
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Barney, Shawn
Thomas, Mary Beth
  33.87%
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6.88%
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ORGANISM: Homo sapiens
                                                                                                     US-09-914-191-1 (1-598)
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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OTHER INFORMATION: Description of Artificial Sequence; No. US20030077587Ale =
OTHER INFORMATION: synthetic construct
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| GlualaaspargaspileMetThrLeualaasnHisTrpasnCysProValLeuSerSer 127
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148 TrpArgAsnMetAsnThrlleLysGlyThrGlnAsnTyrlleProAlaLysCysPheSer
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APPLICANT: Sheffield, Val C.
APPLICANT: Alward, Wallace L.M.
APPLICANT: Fingert, John
TITLE OF INVENTION: GLANCOMA THERAPEUTICS AND DIAGNOSTICS
FILE REFERENCE: 21087.0017U11
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Mismatches:
Indels:
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Matches:
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Matches:
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PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-03-12-15
PRIOR PILING DATE: 1999-08-04
PRIOR PILING DATE: 1999-08-04
PRIOR FILING DATE: 1999-08-04
PRIOR FILING DATE: 1999-08-04
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1997-03-21
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PASLEREQ for Windows Version 4.0
SOFTWARE: 190
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CURRENT FILING DATE: 2001-09-12
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Publication No. US20030077587A1
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76.00
33.70%
26.09%
6.93%
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76.00
                                                              ORGANISM: Homo sapiens
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Query Match:
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                                                                                                                                                                                      Percent Similarity:
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                                                                                    US-09-922-261-375
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Pred. No.:
6core:
SEQ ID NO 375
LENGTH: 488
TYPE: PRT
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718 SerCysGlySerLeuPheProLysAlaLeuGlnArgLeuSerArgSerIleValArgSer 737
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Sequence 144, Application US/09884130

Publication No. US20030055231A1

GENERAL INFORMATION:

APPLICANT: Ni et al.

TITLE OF INVENTION: 12 Human Secreted Proteins
FILE REFREENCE: PF489P2

CURRENT APPLICATION NUMBER: US/09/984,130

CURRENT FILING DATE: 2001-10-29

PRIOR APPLICATION NUMBER: 60/243,792

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-04-18

PRIOR APPLICATION NUMBER: 60/198,407

PRIOR APPLICATION NUMBER: E0/198,071

PRIOR FILING DATE: 1999-10-27

PRIOR FILING DATE: 1999-10-27

PRIOR FILING DATE: 1999-10-28

NUMBER OF SEQ ID NOS: 149

SEQ ID NO 144

LENGTH: 393
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Mismatches:
Indels:
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US-09-914-191-1 (1-598) x US-09-750-240-6 (1-1167)
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                                       TCCCTTCCTTCCCTGTTCCCCTCCCAACTTGAG-
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Matches:
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ORGANISM: Homo sapiens
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Best Local Similarity:
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|110 GluAlaAspArgAspIleMetThrLeuAlaAsnHisTrpAsnCysProValLeuSerSer 129
                                                                                                                                                                                                                                                                                                      --GGTCCGGGTCACTGCCATCTTTTTTCCTTCCAT 403
                                                                                                                                                                                                                                                                                                                                          130 AspSerAspPheCysIlePheAspLeuLysThrdlyPheCysProLeuAsnSerPheGln 149
                                                                                                                                                                                                                                                                                                                                                                                 150 TrpArgAsnMetAsnThrIleLysGlyThrGlnAsnTyrIleProAlaLysCysPheSer 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----CTTCTGCCATAT----
                                                                                                                                                                                                                             GAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTGGCTTTGTCC
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APPLICANT: Insel, P. A.
APPLICANT: Insel, P. A.
APPLICANT: Ping, P.
APPLICANT: Post, S. R.
APPLICANT: Gao, M.
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
TITLE OF INVENTION: PALLURE
FILE REFERENCE: 220002056723
CURRENT APPLICATION NUMBER: US 09/472,667
PRIOR APPLICATION NUMBER: US 09/472,667
PRIOR APPLICATION NUMBER: US 09/008,097
PRIOR APPLICATION NUMBER: US 09/008,097
PRIOR APPLICATION NUMBER: US 09/04,933
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1996-09-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASISED fOR WINDOWS VERSION 4.0
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                                                     Length:
Matches:
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Mismatches:
Indels:
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Matches:
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         416 CTTAATTTCTTTTGTCATCACTTCATCCAC-----
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Gaps:
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                                                     23.5
76.00
33.70%
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Best Local Similarity:
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DB:
US-09-922-261-373
                                     Alignment Scores:
Pred. No.:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                    371
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ORGANISM:
                                                       No.
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	Qy 286 AGCTGTCTTCATCTAGAATCTCTGGATGTTCCTTCCAGAAAGCATCCCGATGATATCGC 345 ::: :::	Qy 346 AGTGCAAGGCACTGGCTTTGTCCTGGTCCGGGTCACTGCCA 387 :::	4-107 07, Appl n No. US PPORMATIO E: Baker, : Beer, : Chen, : Godda	APPLICANT: Pan. James APPLICANT: Smith Victoria APPLICANT: Watanabe, Colin K. APPLICANT: Watanabe, Colin K. APPLICANT: Watanabe, Colin K. APPLICANT: Watanabe, Colin K. APPLICANT: Zhang, Zemin TITLE OF INVENTION: ACIDS ENCODING THE SAME CURRENT FILING DATE: 2002-06-28 CURRENT FILING DATE: 2002-06-28 FILE REPEATOR NUMBER OF SEQ ID NOS: 612 SEQ ID NO 107 LENGTH: 2478 TYPE: DNA ORGANIEM: Homo Sapien US-10-184-644-107	Alignment Scores: 69 Length: 2478 Pred. No.: 73.50 Matches: 29 Score: 75.50 Matches: 29 Percent Similarity: 35.05\$ Conservative: 5 Best Local Similarity: 29.90\$ Mismatches: 18 Query Match: 6.65\$ Indels: 15 DB: 9	357 TGCCTTGCAGTATCATCGGGGATGCTTTCTGGAAGGAACATCCAGAGATTCTAG	Oy 237 CACCTCCCAGGGTCCTTGCCTTAGGTGCTCCCCAGGACACTGGT 178 Db 1157 CysalaThrGlyCysCysalaGGAAGGAGGATGGT 178 Oy 177 GCGAATGACACAACTCAAGTTGGGAGGGAACAGGGAAGGAAGGATGGATGGGT 121 Db 1176 GlyThrGlyThrThrThrThrThrThrThdlyThrAlaGlyAlaGlyAlaCysThrGlyGly 1195 Oy 120 GGTGTATCTTACTCTGTTTAAGCAGAACACCTTGTTTGCGGTGTTGGAACA 70 Db 1196 GlyThrThrThrThrThrThrThrGlyCysCysAlaThrGlyThr 1207 RESULT 13 US-10-184-634-107 ; Sequence 107, Application US/10184634
 	490 GAGCTGCCGATGTATAGGAAAGGGACTGTTGATATGGCAGAAGGTGGATGAAGTGTGTG 431 	430 ACAAAAAATTAAGCTGCCAACAGAAATGGAAGGAAAAGATGGCAGTGACCGGACC 371 	370 AGGACAAAGCCAGTGCCCTTGCACTGCGGATATCATCGGGATGCTTTCTGGAAGGAA	US-09-925-300-1578 US-09-925-300-1578 Sequence 1578, Application US/09925300 Sequence 1578, Application US/09925300 Sequence 1578 Sequence 1578 APPLICANT: Craig Rosen, APPLICANT: Steve Ruben TITLE OF INVENTION: Wucleic Acids, Proteins and Antibodies FILE REFERENCE: PA101 CURRENT APPLICATION NUMBER: US/09/925,300 PRIOR PILING DATE: 2001-08-10 PRIOR PLILING DATE: 2000-03-08 PRIOR PLILING DATE: 2000-03-08 PRIOR PLILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 1890 NUMBER OF SEQ ID NOS: 1890	SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1578 LENGTH: 393 TYPE: PRT TYPE: PRT TYPE: PRT TYPE: STIF LOCATION: (209) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids	Alignment Scores: 28.3 Length: 393 Pred. No.: 75.00 Matches: 29 Score: 39.47% Conservative: 16 Best Local Similarity: 25.44% Mismatches: 45 Query Match: 10 Gaps: 7	US-09-914-191-1 (1-598) x US-09-925-300-1578 (1-393) S9 CCAAAGGAACCATGTTCCAACCACCAAACAAGGTTTACTTTAAACAGAGTAACTAAC

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-----AspThrLysGlyGluAsnile 187
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199 ValGlyLeu-TyrAlaValAlaAlaSerValIleMetArgGlySerSerGlyGlyGlyVa 218
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 584
                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/09910174A Patent No. US20020106730A1 GENERAL INFORMATION:
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73.00
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; LENGTH: 584
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-896-738-18
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Best Local Similarity:
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Best Local Similarity:
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ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 GCGAATGACACAACTCAAGTTGGGAGGGAACA---GGGAAGGAAGGAAGGATGGATGGGTGGT 121
                                                                                                                                                                                                                                                                                                                     APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C217
CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297 ATGAAGACAGCTGACCCTTTTGCGCTTCAGTTGCGTGTGCTTAACCATGCAAGCCCTCC
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Patent No. US20020165347A1
GENERAL INFORMATION:
APPLICANT: Fox, Michael
APPLICANT: Fox, M
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Matches:
Conservative:
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CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 60/215,645
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 18
US20030068684A1
                                                                                                                                                                                                                                                                       Watanabe, Colin K.
Wood, William I.
                                                                                                                                                                 Godowski, Paul J.
Gurney, Austin L.
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35.05%
29.90%
6.65%
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                                                                                                                                     Goddard, Audrey
                                                APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                                                                                                       Pan, James
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Best Local Similarity:
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APPLICANT:
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----ValAlaAspGly 198

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173 ProGlnProGlnIleLysTrpSer------AspThrLysGlyGluAsnIle 187
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                                                                       US20020106730Alel Members of the
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Mismatches:
Indels:
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APPLICANT: Coyle, Anthony J.
APPLICANT: Fraser, Christopher C.
APPLICANT: Manning, Stephen
TITLE OF INVENTION: B7-H2 Molecules, No. US2002
TITLE OF INVENTION: Family and Uses Thereof
FILE REFERENCE: 35800/236924
CURRENT PAPLICATION NUMBER: US/09/910,174A
CURRENT FILING DATE: 2000-07-20
PRIOR APPLICATION UNMBER: US 09/620,461
PRIOR FILING DATE: 2000-07-20
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ò	302 AATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACT 359	
ą	::: 236 rileAlaAspProPhePheArgSerAlaClnProTrpileAlaAlaLeuAlaGlyThr 255	

Search completed: July 9, 2003, 12:53:09 Job time : 39 secs

prote

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secretion

Title: Perfect score:

Sequence:

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Scoring table:

Total number

Searched:

8 0 0 0

Minimum I Maximum I

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A;Cross-references: EMBL:AL049522; PIDN:CAB40011.1; GSPDB:GN00068; SPDB:SPCC63.07
A;Experimental source: strain 972h-; cosmid c63
                                                                                                                                                                              hypothetical prote
gene forked protei
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RNA-binding protei
polyprotein (clone
nitrogenase iron-m
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                                                                                                                                    probable membrane
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 15-Sep-2000
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| LysHisGluIleLeuPheSerLysPheGlyIleAsnTyrAsnPheGluProGluIleTyr
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                                                                                                                                                           hypothetical
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                                                                                                             general
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R;Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, submitted to the EMBL Data Library, March 1999
A;Reference number: Z21999
A;Accession: T41508
A;Accession: T41508
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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38
32
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Matches:
Conservative:
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 T18274
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S64925
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T117171
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S76065
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A;Introns: 79/2; 179/3; 214/3
                                   1-261 <MUR>
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Best Local Similarity:
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                                                             Alignment Scores:
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-MODEL=frame+ n2p.model -DEV=xlp
-Q=CQGD2_11/02FTO_SODO_1/020914191/runat_09072003_112350_12889/app_guery.fasta_1.775
-Q=CQGD2_11/02FTO_SODO_1/0209914191/runat_09072003_112350_12889/app_guery.fasta_1.775
-QGD2_11/02FTO_SODO_1/0209914191/runat_09072003_1-LOOPCID=0 -LOOPEXT=0
-UNITS=Bits -STRAT=1 -END=-1 -MATRIX=bloounm62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL.
-USTRYT=pct -NORM==xt -HERASIZE=500 -MINLEND=0 -MAXENE=200000000
-USTR=-USCOS914191 @CGN 1 1 62 @runat_09072003_112350_12889 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQÜERY -NEG SCORES=0 -WAIT -DSPBLOCK=I00 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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membrane-bound lyt
                                                                                 ; Search time 25 Seconds (without alignments) 4599.071 Million cell updates/sec
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                                                                                                                                                           598
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                                                                                                                                                         ttggaatagttcttgcttta......ggtgttagtccagattgttg
            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                           protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                              hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                 9, 2003, 12:46:18
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S64315
G84731
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T51779
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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205

169.5 122 122 94 90 83.5 83.5 82.5 81.5 81.5

2500

80. 78.

Score

No. Result

Database

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hypothetical protein At2g31580 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Decies: Arabidopsis thaliana (mouse-ear cress) C;Species: Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: E8472. R. R. Roul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. Nature 402, 761-768, 1999 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               535 AAGAATGAGATTTTGTTTTTCTGAATTCAACATCAACTATAATAATGAGCTGCCGATGTAT 476
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394 LysSerGlyLysAsnLysThrGlnSerGlnAspTyrLeuLysGlyThrGlnThrArgGlu 413
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                    A;Molecule type: DNA
A;Residues: 1-297 <STO>
A;Croser references: GB:AE002093; NID:g3831463; PIDN:AAC69945.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g32330
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A;Residues: 1-457 <STO>
A;Cross-references: GB:AE002093; NID:g4582470; PIDN:AAD24854.1; GSPDB:GN00139
C;Genetics:
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Best Local Similarity:
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A;Status: preliminary
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A,Map position: 2
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NyAlternate names: hypothetical protein G4041
C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 19-Apr-2002
C;Accession: S64315
R;Rieger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.
Bubmitted to the Protein Sequence Database, May 1996
A;Reference number: S64071
A;Accession: S64315
A;Acc
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C.Species: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 17-May-2002
C.Accession: G84731
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul, S.; Rronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                          239 IleLeuHisValSerLeuIleAspAspAspPheTrpThrSerArgProPheLeuGluVal 258
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Superfamily: Saccharomyces cerevisiae hypothetical protein YGR024c
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: F96524
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, Bi6-820, 2000
A;Authors: Hunter, J.L.; Jin, X.; Liu, X.; Liu, Z.A.; Luros, J.S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                            362 CTTTGTCCTGGTCCGGGTCACTGCCATCTTTTTCCTTCCATTTCTGTTGGCAGCTTAAT 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 GGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGAGGCCTTGCATGG 252
                                         AATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTGG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 TTAAGCACACCAGAAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTAGAATCTCTGGAT 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----LeuLeuTrp 49
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---AsnLysProGlnLeuSerArgValArgValAlaCysSerSerSerGlnSerAspSer 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB: AE005173; NID: 98778686; PIDN: AAF79694.1; GSPDB: GN00141
                                                                                                                                                        TICTITIGICACTICACCACCTICIGCCATAT------
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18
62
65
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Conservative:
Mismatches:
Indels:
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JS-09-914-191-1 (1-598) x S54157 (1-279)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 SerArgGlnThr-----
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33.16%
23.68%
7.53%
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A;Molecule type: DNA
A;Residues: 1-343 <STO>
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Best Local Similarity:
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R; Arsenijevic-Maksimovic, I.; Broughton, W.J.; Krause, A.
submitted to the EMBL Data Library, April 1995
A; Description: A class of root-hair specific extensins involved in rhizobium/legume inte
A; Reference number: S54155
A; Accession: S54157
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ω
                                                                                                   C;Accession: JE0212
R;Hagiwara, K.; Tomita, M.; Kobayashi, J.; Miyajima, S.; Yoshimura, T.
Biochem. Biophys. Res. Commun. 247, 549-553, 1998
A;Title: Nucleotide sequence of Bombyx mori cytoplasmic polyhedrosis virus segment
A;Reference number: JE0211; MUID:98321164; PMID:9657006
                                         H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAATGGAAGGAAAAAAAGATGGCAGTGACCCGGACCAGGACAAAGCCAGTGCCCTTGCAC 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               517 TCTGAATTCAACATCAACTATAATAAT-----GAGCTGCCGATGTATAGGAAAGGG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       466 ACTGTGTTGATATGGCAGAAGGTGGATGAAGTGACAAAAGAAATTAAGCTGCCAACA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 AspMetGlu------ValAlaThrProLysValLeuGluProProThrProLeuPro 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     346 TGCGATATCATCGGGGATGCTTTCTGGAAGGAACATCCAGAGATTCTAGATGAAGACAGC 287
                                       Pothetical 44k protein - Bombyx mori cytoplasmic polyhedrosis virus strain Species: Bombyx mori cytoplasmic polyhedrosis virus, BmCPV Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-390 <HAG>
A;Cross-references: GB:AB016437; NID:g3395152; PIDN:BAA32043.1; PID:g3395153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        extensin-like protein - cowpea (fragment)
C;Species: Vigna unguiculata (cowpea)
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 03-Aug-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 279
Matches: 21
Conservative: 9
Mismatches: 23
Indels: 3
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227
24
8
8
8
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Matches:
Conservative:
Mismatches:
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                                         hypothetical 44k protein - Bombyx mori
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85.00
50.00%
26.47%
7.69%
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83.50
41.67$
29.17$
7.62$
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231 LeuPro 232
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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A;Residues: 1-279 <ARS>
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Pred. No.:
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Db 69 ArgProGluLysLysGlnSerAspLysSerAsnTyrAlaArgAlaGluLeuPheArgGly 88	0.60 プランエック もつうごかい プラジ はいかい はんせいかい かいかい かいかい かいかい かいかい かいかい からっかっしょう しゅっしょう しゅうしょう しゅうしゃ しゃくりん しゅうしゃ しゅうしゃ しゅうしゃ しゅうしゃ しゃくりん しゃくりん しゃく しゅうしゃ しゃくりん しゃく
370 TGGTCCGGGTCA 38	231 PheLysProPheCysLeuLeu-ProCysGlnMetSerHisSerTh 24
50	, Qy 229 AGGGCTCCTTGCCTTAGGT
Ογ 381 381	Db 245 ranglulenVallenAlaValTvrIvsGlvAspArgPheSerLenLenLvsGlnCvsSe 265
Db 109 ValSerAlaProPheGlnGluGluLysGlySerPheLeuTrpValLeuAlaProValVal·128	202 CATCCCTACCACCACCACCACCACCACCACCACCACCACCA
Qy 382	265 rValThrArgGluIleGlyValTrpValThrLysGluArgIleSerAsnAsp
CTTTTGFCATCACTTCACCTTCTGCCATATCAACACAGTCCCTT 47	Qy 160 AGTIGGGAGGGAACAGGAAGGAAGGATGGATGGGGGGGGGG
Db 149 LysAsnAspThrValAlaGlyArgSerGluIleValThrSerPheCysPheGluThrVal 168	283AsnGlyAsnGlyGlyGluGlyValGlu-TrpLeuLysLeuMetThrLeuSerL
Qy 472 TCCTATACATCGGCAGCTCATTATAGT 501	OY 100 AGCAGAACACCTTGTTTGCGGTGTTGGAACATGGTTCCTTTGGCAAGTGCTT 4/
Db 169 PheTyrAlaGlyLeuAlaIlePheLeuSer 178	46 TT 45
REGULT 8 784550 hydotherical profein At2017310 (immorfed) - Arabidonsis thaliana	320 yr
C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001	
C;Accession: F84550 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.	non-phototropic hypocotyl 3-like protein - Arabidopsis thaliana N.Alternate names: protein F28bl0_10_10 C;Species: Arabidopsis thaliana (mouse-ear cress)
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, d Nature 402, 761-768, 1999	C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000 C:Accession: T51779
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197	R;Delseny, M.; Berger, C.; Cooke, R.; Grellet, F.; Laudie, M.; Mewes, H.W.; Rudd, S.; L submitted to the Protein Sequence Database, August 2000
A;Accession: F84550 A;Status: preliminary	A;Reference number: Z25454 A;Accession: T51779
A;Molecule type: DNA A;Residues: 1-370 <sto></sto>	A;Status: preliminary A;Molecule type: DNA
A;Cross-references: GB:AE002093; NID:g2262162; PIDN:AAB86508.1; GSPDB:GN00139 C;Genetics:	A;Residues: 1-661 A;Cross-references: EMBL:AL391254
A;Gene: At2g17310 A;Map position: 2	A;Experimental source: cultivar Columbia; BAC clone F28D10 C;Genetics:
C; Superfamily: Arabidopsis thaliana hypothetical protein F24M12.210	A;Map position: 3 A:Infrons: 28/3: 83/3: 419/3
Length:	A,Note: F28D10_10 C;Superfamily: Arabidopsis hypothetical protein F19F18.80
t Similarity: 38.12% Conservative:	Alignment Scores:
23.278 7.388 2	4.21 Length: 81.50 Matches: 41.34% Conservative:
(0 (1-370)	Best Local Similarity: 25.14* Mismatches: 62 Query Match: 7.38* Indels: 43
Oy 520 TTTCTGAATTCAACATAATAATAATGAGCTGCCG	-09-914-191-1 (1-598) x T51779 (1-661)
	505 AICAACTATAATAAGGCTGCCGATGTATAGGAAAGGGACTGTG
Db 154 GlyHisLeuPheCysHisGlyLysValLeuArgAspGlnLysValValIleTyrGluCys 173	398 LeudsnifyrSerdspSerGluThrLeuTyrAsnValAspCysValGluArglieValArg
433 ATGACAAAAGAAATTAAGCTGCCAACAGAAATGGAAAAAAAA	OY 460 TROMINGGROUNGSTOND 413 Db 418 HisPheTrpArgLeuValAspSerTyrMetAlaGluValAlaSerAspValAsnLeuLys 437
174 AlaSerAspSerLeuArgPheIleAspArgProGluAspAspAspTrpProIleThrGlu	Qy 412 CCAACAGAAATGGAAAAAAAAAAAGATGGCAGTGACCCGGACCAGGACAAAGCCAGTGCCC 353
<pre>dy 373 ACCAGGACAAAGCCATGCACTGCACTGCGATGCTGGGATGCTTTCTGG 320</pre>	::: aAlaAlaLeuProGluSerSerArgPro
319GAAGAACATCCAGAGATTCTAGAT	Oy 352 TTGCACTGCGATATCATCGGGGATGCTTCTGGAAGGACATCCAGAGATTCTA 299
'Db 211 CysSerAsnTyrGluAsnAspGluTyrTyrIleArgilePheAspPheSerThrGluAsp 230	

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A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 [Accession: AF2172 R;Accession: AF2172 R;Accession
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A;Reference number: Z18876
A;Reference number: T318319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- ACCACCCAGGACACTGGTGC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGCTGCCA---ACAGAAATGGAAGGAAAAAAAGATGGCAGTGACCGGACCAGGACAAAG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTA-----GATGAAGACAGCTGA 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProAlaThrGlySerIleAsnValProValThrProGluArgSerIleAlaThrAspLys 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          352 aGlyGlyArgMetGluTyrArgThrValSerArgTyrValLeuAspĠinAspThrGly-- 371
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-AsnalaIleLysGlyProGlyArgValAspTyrPheMetGlyThrGlyLysGlnAlaGl 391
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C;Species: Leishmania major
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2002
C;Accession: T1819
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C;Species: Nostoc sp.
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Hagiwara, K.; Tomita, M.; Kobayashi, J.; Miyajima, S.; Yoshimura, T.
iochem. Biophys. Res. Commun. 247, 549-553, 1998
Title: Nucleotide sequence of Bombyx mori cytoplasmic polyhedrosis virus segment 8.
Heference number: JE0211; MUID:98321164; PMID:9657006
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PheGluGlnMet-HisLeuArgThrAlaLeuAla---GlyGlyLeuAsnValAlaAsnTh
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A;Status: preliminary; translated from GB/EMBL/DDBJ *Molecule type: DNA A;Resiques: 1-320 <011>	Score: Similarity: 37. Best Local Similarity: 23.
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ent Scores: 7.17 Length:	US-US-914-191-1 (1-598) X T Qy 220 AAGGAGCCCTGGG
Score: 79.00 Matches: 44 Percent Similarity: 31.98 Conservative: 11	
: 25.56% Mismacches: 7.21% Indels: 2 Gaps:	Qy 253 TTAAGCACAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
US-09-914-191-1 (1-598) x T18319 (1-320)	123
78 CACCGCAAACAAGTGTTCTGCTTAAACAGAGTAAGATACACCACCCCCAT	OY 313 GITCLICCRGARA Db 148 ePhe
69 HisArgArgLeuCysSerLeuLeuSerLeuLeuLeulleHisThrHisProHisIleThr	Qy 373 TCCGGGTCACTGC
UY 128	Db 154 yProSerThrCys
129CDATCCCTTCCTTCCCTCCTCCCTCCTCCCTCCTCCCTCC	Qy 421 TTTCTTT
	174
Qy 156 CAACTIGAGTIGIGATTCGCACCAGIGICCIGGGIGGIAGGAAIGCIACAGCCACCTA 215	463
Db 129 ArgLeu 132	194
Qy 216 AGGCAAGGAGCCCTGGGAAGGTGGGAGGCTTGCATGGTTAAGCACACCAGAACT 269	523
133	203 oGluPheSer
Qy 270 GAAGCGCAAAAGGGTCAGCTGTCTTCATCTAGAATCTCTGGATGTTCCTTCC	RESULT 14 H84071
Db 146 AlaGlyArgLysGlyGlnIleAlaArgGluArgArgLysGlyThrGlyArgArgAsp 165	lipopolysaccharide biosynth C;Species: Bacillus halodur
QY 330 TCCCCGATGATATCGCAGTGCAAGGGCACTGGCTTTGTCCTGGTCCGGGTC 380	C;Date: U1-Dec-2000 #sequen C;Accession: H84071
Db 166 GlyProSerProProSerCysAlaCysPheSerPheValLeu-SerValAlaGluThrTh 185	Nicleic Acids Res. 28, 4317
Qy 381 ACTGCCATCTTTTTCCTTCCATTTCTGTGGCAGCTTAATTTCTTTTGCATCA 440	A;Itte: Complete genome se A;Reference number: A83650; A;Accession: H84071
Db 185 rLeuProProMetArgSerProSerAlaProProLeuLeuLeuSerProProPr 203	A.Status: preliminary A.Molecule type: DNA
Qy 441 TCCACCTTCTGCCATATCAACACGTCCCTTTCC 474	A;Residues: 1-397 -STO> A;Cross-references: GB:AP00 A;Experimental source: stra
SULT 13	C;Genetics: A;Gene: BH3376
T31614 hypothetical protein Y50E8A.j - Caenorhabditis elegans C.Snerias Canorhabditis alegans	Alignment Scores:
C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C.Accession: T31614	Score: 78. 78. Percent Similarity: 40.
R.Steward, C. Bubmitted to the EMBL Data Library, September 1999 A:Reference number: Z21047	
A.Accession: T31614 A.Status: preliminary: translated from GB/EMBL/DDBJ	US-09-914-191-1 (1-598) x H
A; Residues: 1-225 VVIL. A; Residues: 1-225 VVIL. A; Residues: 1-225 VVIL.	Oy 19 TATAAAAATAGTA
A,twoss references: mmb.:hull/200; Nib:el349/70; FibN:CAB33033.1; CESF:130E0A.] A,FEDETimental source: clone Y50E8A C.Genetics:	Db 149 TrpLysTyrSerT
A;Gene: CESP:Y50E8A.j	Oy 58 CCAAAGGAACCAT
Alignment Scores: 7.8 Length: 225	Db 169 ProSerAsnTrpL

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.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir: 17-4331, 2000
sequence of the alkaliphilic bacterium Bacillus halodurans and ); MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  001518; GB:BA000004; NID:g10175792; PIDN:BAB07095.1; GSPDB:GNO:
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|sasnValPheSerIleTrpProGlnTrpAsnPheGlyAsnSerAsnAs 174
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ThrGluPheGluSerArgAlaLeuSerGluSerGlnHisIleIleThr 168
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------AlaAsnLeuGlnPheArgLeuPr 203
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Oy 274 GCTTCAGTTCTGGTGGCTTAACCATGCAAGCCTTCCAGGGCTCCTTGCCTT 215 Db 595ArgLysLeuArgGluLeuAlaMetLeuAlaLysProGlnSerAsnValProAlaAla 613 Oy 214 AGGTGGCTGTAGCATCCCTACCAGCACACTGGTGCGAATGACACACAC	Qy 97 AGAACACCTTGTTTGCGGTGTTGGAAC	arch complet b time : 30			
Qy 118 ACCACCCCCATCCATCCTTCCTTCCTTCCTTCCTTCCTT	Oy 226 CCCTGGGAGGTGGAGGCTTGCATGGTTAAGCACCCAGAACTGAAAGG 282 Db 248 AspTrpGluCysTrpPhe11eGlyAsnGlyGlu11eivgLysLeu 263 Oy 283 GTCAGC 288 I ::: Db 264 ValAsn 265	linositc tryoscel 1-1939 # 1-1939 # akegawa, akegawa, 11. 15, akegawa, 11. 18, akegawa, 11. 18, akegawa, akea akea akea akea akea akea akea ak	H :		Qy 451 CAGAAGGTGGATGACAAAAGAAATTAAGCTGCCAACAGAAATGGAAGGAA

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=S288c;
MEDLINE=97435481; PubMed=9290212;
Riger M., Brueckner M., Schaefer M., Mueller-Auer S.;
"Sequence analysis of 203 kilobases from Saccharomyces cerevisiae chromosome VII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YGIG YEAST STANDARD; PRT; 237 AA.
P53215;
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical 27.8 kDa protein in VMA7-RPS25A intergenic region.
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                         Y966 TREPA
MNT MOUSE
MYOC RAT
POLG HCVJA
AGLA RHIME
PTPX MACNE
POLG HCVTW
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SKIL, HUMAN
HOCI_YEAST
ILVD_AGRTS
ODDB_PORPU
ONOS_CHICK
PRO_CHICK
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-!- SIMILARITY: TO S.POMBE SPCC63.07.
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                         NCBI_TaxID=4932;
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SEQUENCE 23
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  MODEL=frame+ n2p. model - DEV=xlp  
-Q=/cgn2_1/USPTO_spool/US09914191/runat_09072003_112348_12866/app_query.fasta_1.775  
-D==SwissProct 40 - QFW=fasta_n - GFFTX=rsp - MINNATCH=0.1 - LOODCL=0 - LOOPEXT=0 - MAXLEN=200000000 - LOOPEXT=0 - LOOPEXT=0 - MAXLEN=200000000 - LOOPEXT=0 - LOOPEXT=0 - MAXLEN=200000000 - LOOPEXT=0 - LOOPEXT
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                 GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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FXO3_HUMAN
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P3K3_DICDI
DTNB_MOUSE
DINA_HUMAN
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Listing first 45 summaries
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                                                                                  GGACTAACACCAGTACAAGCCCAAGGGAGATTACAGGGAACTCTTNCAGCAGACAAGAAT 530
                                                                                                         -!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
-!- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- ALTERNATIVE PRODUCTS: 2 ISOPORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, HEART, VAS DEFERENS, KIDNEY. SKELETAL MUSCLE, THYMUS, LUNG AND SPLEEN. WEAK EXPRESSION
                                                                                                                                                                         GAGATTTTGTTTTCTGAATTCAACATCAACTATAATAATGAGCTGCCGATGTATAGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brain Res. Mol. Brain Res. 73:85-92 (1999).
-!- FUNCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYZE ATP AND OTHER NUCLECTIDES TO REGULATE PURINERGIC NEUROTRANSMISSION. HYDROLYZES ADP ONLY TO A MARGINAL EXTENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOPORM 1), AND CHARACTERIZATION.
STRAIN=Sprague-Dawley, TISSUE=Brain;
MEDLINE=98031057; PubMed=9364474;
Kegel B., Braun N., Heine P., Maliszewski C.R., Zimmermann H.;
"An ecto-ATPase and an ecto-ATP diphosphohydrolase are expressed in rat brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INDUCTION: BY FSH IN SERTOLI CELLS BUT NOT IN PERITUBULAR CELLS; BY CAMP IN BOTH TYPE OF CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vlajkovic S.M., Housley G.D., Greenwood D., Thorne P.R.; "Evidence for alternative splicing of ecto-ATPase associated with termination of purinergic transmission.";
                                                                                                                                                                                                                                                                                                                                                                                           ENP2_RAT STANDARD; PRT; 495 AA.
035795; Q9MYB7;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
18-OCT-2001 (Rel. 40, Last sequence update)
18-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cells.";
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SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=Sprague-Dawley; TISSUE=Sertoli cells;
MEDLINE=21121474; PubMed=11229804;
Lu Q., Porter L.D., Cui X., Sanborn B.M.;
"Ecto-ATPase mRNA is regulated by FSH in Sertoli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 379-495 FROM N.A. (ISOFORM 2)
STRAIN=Wistar; TISSUE=Cochlea;
MEDLINE=20050856; PubMed=10581401;
Gaps:
                           US-09-914-191-1 (1-598) x YG1G_YEAST (1-237)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neuropharmacology 36:1189-1200(1997)
                                                                                                                                                                                                                                                                                    ||||::::::::
|||SerLeuVal 215
                                                                                                                                                                                                                                                              GGGACTGTGTTG 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PheTyrTyr-----ThrValAspPheLeu------ThrThrValMetGlyLeuPro 362
                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . . ) (POTENTIAL).

N-LINKED (GLCNAC. . . ) (POTENTIAL).

N-LINKED (GLCNAC. . . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 LeuleuAlaSerAlaLeuGlnileHisArgPheHisProCysTrpProLysGlyTyrSer 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272 ThrGinValLeuLeuGlnGluValTyrGlnSerPro-------CysThrMetGly 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 GCGCAAAAGGGTCAGCTGTCTTCATCT----AGAATCTCTGGATGTTCCTTCCAGAAA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGAATTCAGAAAACAAAATCTCATTCTTGTCTGCTGNAAGAGTTCCCTGTAATCTCCCT 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 TCCCAACTTGAGTTGTGATTCGCACCAGTGTCCTGGGTGGTAGGGATGCTACAGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      288 GlnArgProArgAlaPheAsnGlySerAlaIleValSerLeuSerGlyThrSerAsnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387 ATCTTTTTCCTTCCATTTCTGTTGGCAGCTTAATTTCTTTTGTCATCACTTCATCCACC
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                                                                                                                                                                                                                                                         Hydrolase; Transmembrane; Glycoprotein; Calcium; Magnesium;
                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF -> LL (IN REF. 2).
A -> T (IN REF. 2).
L -> F (IN REF. 2).
c 237B999F1BEBBBEOO CRC64;
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222
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933
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Matches:
Conservative:
Mismatches:
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T -> A (IN REF.
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                                                                                                                      US-09-914-191-1 (1-598) x ENP2_RAT (1-495)
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                                                                                         EMBL; Y11835; CAA72533.1;
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85.50
39.13%
25.47%
7.80%
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363 ValGlyThrLeuLysGlnLeuGlu-----GluAlaThrGluIleThrCysAsnGlnThr 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa M., Nishia K., Kiyosawa H., Kondo S., Yamanaka I., Asito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Rieschmann W., Gasserand T., Gissi C., King B., Kochiwa H., Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Balake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., A., Liyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sato K., Schoenbach C., Seya T., Shibata Y., Storich K.-F.,
                                                                                                                                                                                                                                                                                                                                                                                                    mouse gene with homology to ecto-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THE 409:685-690(2001).

FUNCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYZE ATP AND OTHER NUCLEOTIDES TO REGULATE PURINERGIC NEUROTRANSMISSION. HYDROLYZES ADP ONLY TO A MARGINAL EXTENT (BY SIMILARITY).

CATALYTIC ACTIVITY: ATP + H(2)0 = ADP + phosphate.

COFACTOR: REQUIRES CALCIUM AND MARGHESIUM.

SUBGELLULAR LOCATION: Integral membrane protein (Potential).

ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                      ENP2 MOUSE STANDARD; PRT; 495 AA.
055026; 035928; 99DCR9;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ecconucleoside triphosphate diphosphohydrolase 2 (EC 3.6.1.3)
(NTPDase2) (Ecto-ATPase) (CD39 antigen-like 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gao L., Dong L., Whitlock J.P. Jr., "A novel response to dioxin. Induction of ecto-ATPase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: HAS PROBABLY DISULFIDE BONDS.
SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. INDUCTION: BY DIOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning and mapping of a human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem. 273:15358-15365(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Kidney;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Hepatoma; MEDLINE=9624117; MEDLINE=9828117;
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97419269; PubMed=9271669;
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (SHORT FORM).
                                                                                                                                                                                                                                                                                                                                                                                   Chadwick B.P., Frischauf A.-M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (LONG FORM).
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                                                                                                                                                                                                                                                                                                                                                                                                               ATPase genes.";
Mamm. Genome 8:668-672(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409:685-690(2001)
                                                                                                                                                                                                                                                       Wus musculus (Mouse)
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                             TGG 569
                                                        Trp 381
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                                                                                                                                                                                                                                                                                                                                                  TISSUE=Embryo;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286 MetGlyGlnArgProGlnThrPheAsnSerSerAlaThrValSerLeuSerGlyThrSer 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321 CAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTGGCTTTGTCCTGGTCCGGGTC 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381 ACTGCCATCTTTTTCCTTCCATTTCTGTTGGCAGCTTAATTTCTTTTGTCATCACTTCA 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCACCTTCTGCCATATCAACACAGTCCCTTTCCTATACATCGGCAGCTCATTATTAG 500
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270 TyrSerThrGlnValLeuLeuArgGluValTyrGlnSerPro--------CysThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 GlnArgLeuLeuAlaSerAlaLeuGlnIleHisArgPheHisProCysTrpProLysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 TTCCCCTCCCAACTTGAGTTGTGTCATTCGCACCAGTGTCTGGGTAGGGATGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 AGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGAGGCTTGCATGGTTAAGCACACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 AsnAlaAlaLeuCysArgAspLeuValSerGlyLeuPheAsnileSerSerCysProPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267 ACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCT-----AGAATCTCTGGATGTTCCTTC
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N-LINKED (GLCNAC. .) (POTENTI
LTS -> MAG (IN SHORT ISOFORM).
MISSING (IN SHORT ISOFORM).
T -> A (IN REF. 3).
S -> R (IN REF. 3).
T -> A (IN REF. 3).
T -> A (IN REF. 3).
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                                                                                                                                                                                                                                   PROSITE: PS01238; GDAI_CD39 NTPASE; 1.
Hydrolase; Transmembrane; Glycoprotein; Calcium; Magnesium;
                                                                                                                                                                                                                                                                                                                     POTENTIAL.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
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                                                                                                                                                                                 MGD; MGI:1096863; Entpd2.
InterPro; IPR000407; GDA1 CD39 NTPase.
Pfam; PF01150; GDA1 CD39; 1.
                                                                                                                                           EMBL; AF042811; AAC24347.1; -. EMBL; AK002553; BAB22182.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ψ.
                                                                                                                               EMBL; U91511; AAB81014.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                437
54310
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84.50
37.80%
25.61%
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44
462
493
129
294
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132
495
                                                                                                                                                                                                                                                                                Alternative splicing.
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495 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity:
                                                                                                                                                                                                                                                                                                                                                                                          64
129
294
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130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
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                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
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                                                                                                                                                                                                                                                                                                   DOMAIN
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SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: UBIQUITOUS.
PTH: PHOSPHORYLATED BY AKTI.
DISBASE: INVOLVED IN A T(6;11) (Q21;Q23) CHROMOSOMAL TRANSLOCATION
IN SECONDARY ACUTE LEUKEMIA THAT INVOLVES FOXO3A AND MLL.
SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
DATABASE: NAME-ARIBS Genet. Cytogenet. Oncol. Haematol.;
WWW*"http://www.infobiogen.fr/services/chromcancer/Genes/AF6q211D125.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                 FXO3 HUMAN STANDARD; rki; v, r...
043524; O15171;
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 41, Last sequence undate)
15-UJW-2002 (Rel. 41, Last annotation update)
Forkhead box protein O3A (Forkhead in rhabdomyosarcoma-like 1) (AF6q21
                                                                                                       68 LeuAlaProTyrIleLysAsnHisLeuValAlaSerAsnAspLysGluValPheAlaLeu
                                                                                                                                            -------AAAGAAATTAAGCTGCCAACAGAAATGGAAGGAAAAAAGATGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hillion J., Le Coniat M., Jonveaux P., Berger R., Bernard O.A.;
"AF6G21, a novel partner of the MLL gene in t(6;11)(q21;q23), defines a forkhead transcriptional factor subfamily.";
Blood 90:3714-3719(1997).
-!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR THAT MAY TRIGGER APOPTOSIS BY INDUCING THE EXPRESSION OF GENES THAT ARE CRITICAL
                                                                                                                                                                                                                GTGACCCGGACCAGGACAAAGCCAGTGCCCTTGCACTGCGATATCATCGGG-----
                                                                       --GATGAAGTGATGACA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=98140118; PubMed=9479491; Anderson M.J., Viars C.S., Czekay S., Cavenee W.K., Arden K.C.; "Cloning and characterization of three human forkhead genes that comprise an FKHR-like gene subfamily."; Genomics 47:187-199(1998).
CTGCCGATGTATAGGAAAGGGACTGTGTTGATATGGCAGAAGGTG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                       331 GATGCTTTCTGGAAGGAACAT 311
                                                                                                                                                                                                                                                                                                                       126 GlySerAlaTrpLysGluTyr 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-383 FROM N.A.
MEDLINE=98008138; PubMed=9345057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FOR CELL DEATH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOXO3A OR FKHRL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                       442
187
                                                                                                                                            427
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                                                                                                                                                                                                                                                                                                                                                                                 FXO3_HUMAN
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 GGACTAACACCCAGGACCCCAAGGGAGATTACAGGGAACTCTTNCAGCAGGACAAGAAT 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       529 GAGATTTTGTTT--------TCTGAATTCAACATCAACTATAATAATGAG 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :::|||||||
AsnLeuLeuPheValAlaThrAspArgIleSerAlaTyrAspValIleMetThrAsnGly 49
                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phosphoribosylamidoimidazole-succinocarboxamide synthase (EC 6.3.2.6)
(SAICAR synthetase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 263:155-169(2001).
-!- CATALYTIC ACTIVITY: ATP + 5-amino-1-(5-phospho-D-16osph) imidazole-4-carboxylate + L-aspartate = ADP + phosphate ($\sigma^2 - [5-amino-1-(5-phospho-D-ribosyl)] imidazole-4-carboxamido]succinate - i-pathway: De novo purine biosynthesis; seventh step.
-!- PATHWAY: BELONGS TO THE SAICAR SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21125227; PubMed=11223254;
Lin Cereghino G.P., Lin Cereghino J., Sunga A.J., Johnson M.A.,
Lim M., Gleeson M.A.G., Cregg J.M.;
"New selectable marker/auxotrophic host strain combinations for
molecular genetic manipulation of Pichia pastoris.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34101 MW; 584073DA712262C9 CRC64;
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23
37
38
6
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Matches:
Conservative:
Mismatches:
Indels:
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Pfam; PF01259; SAICAR synt; 1.
Probom; PD003043; SAICAR synt; 1.
TIGRFAMS; TIGR00081; purG; 1.
PROSITE; PS01057; SAICAR SYNTHETASE 1; 1.
PROSITE; PS01058; SAICAR SYNTHETASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-914-191-1 (1-598) x PUR7_PICPA (1-304)
                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Purine biosynthesis
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80.00
40.94%
22.83%
7.24%
                                                  561 CTCCCTTGGGCT 572
                                                                                      379 GlnThrŤrpAja 382
                                                                                                                                                                                                                                                                                                          Pichia pastoris (Yeast).
                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ä
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                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P27616;
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Q9C1J4;
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                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FALSE_NEG.
FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00649; G PROTEIN RECEP F2 1;
PS00650; G PROTEIN RECEP F2 2;
PS50227; G PROTEIN RECEP F2 3;
                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AB011529; BAA88687.1; -.
HSSP; P00740; IEDM.
InterPro; IPR001529; Aax hydroxyl.
InterPro; IPR00156; Cadherin.
InterPro; IPR001561; EGF-like.
InterPro; IPR00181; EGF-Za.
InterPro; IPR00181; EGF-Za.
InterPro; IPR00181; EGF-Za.
InterPro; IPR00183; EGF-II.
InterPro; IPR00193; Hormi receptor.
InterPro; IPR00193; hormi receptor.
InterPro; IPR001791; Laminin EGF.
InterPro; IPR001791; Laminin GG.
InterPro; IPR001791; Laminin GF.
Pfam; PF000023; PRD_Cys_rich.
Pfam; PF000023; PRD_Cys_rich.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWART; SW00112; CA; 3.
SWART; SW00179; EGF CA; 1.
SWART; SW00010; EGF Like; 6.
SWART; SW00001; GPS; 1.
SWART; SW00009; HormR; 1.
SWART; SW00009; HormR; 1.
SWART; SW00028; LamG; 2.
PROSITE; PS00010; ASX HYDROXYL; 2.
PROSITE; PS00032; CADHERIN 1; 3.
PROSITE; PS50268; CADHERIN 2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPS; 1. _
LAM G DOMAIN; 2.
EGF_1; 6.
EGF_2; 4.
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GPCRSECRETIN
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PRINTS; PR00205; CADHERIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF02793; HRM;
                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS, PR00205; C PRINTS, PR00010; F PRINTS, PR00011; F PRINTS; PR00249; C
                                               NCBI_TaxID=10116;
    CELSR2 OR MEGF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
   -----GlnGlyAlaLeuGlyGlySerArgAlaLeu-----SerAsn 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerValSerAsnMetGlyLeuSerGluSerSerSerLeuGlySerAlaLysHisGlnGln 572
                                                                                           -> AWQPHUNAANSWWRGRTSVHAPILTPAGSVAACRFSW
QV (IN REF. 3).
PMLYSSSAGLSPSVSKP -> AHALQHVSQPVTFSKQA
(IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 TTCCCCTCCCAACTTGAGTTGTGTCATTCGCACCAGTGTCCTGGGTGGTAGGGATGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 AGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGAGGCTTGCATGGTTAAGCACACAGA
                                                                                                                                                                                                                             AWGNLSYA -> WGKPUYS (IN REF. 3).
PDGGKGGKA -> LWGEERKT (IN REF. 3).
S -> T (IN REF. 3).
MISSING (IN REF. 3).
PGSSPTGRSSDELDAWTDFRSRTNSNASTVSGRLSPIMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327 GCATCCCCGATGATATCGCAGTGCAAGGGCACTGGCTTTGTCCTGGTCCGGGTCA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cadherin EGF LAG seven-pass G-type receptor 2 (Multiple epidermal
growth factor-like domains 3) (Fragment).
                                                                                                                                                                                                                                                                                                                                                        LT -> AD (IN REF. 3).
E5B4E830665A9982 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      673
27
13
26
33
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Matches:
Conservative:
Mismatches:
Indels:
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D -> E (IN REF. 3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-914-191-1 (1-598) x FXO3_HUMAN (1-673)
L; BC021227; A-102271; -.
L; BC021224; AAH12224.1; -.
L; AJ001589; CAA04860.1; -.
;; AJ001590; CAA04861.1; -.
;; C63245; ZHFH.
                                                                                                                                                                                                                                                                                                                                                                      71276 MW;
                                                                 TRANSFAC, T02938;
Genew; HGNC:3821; FOXO3A.
                                                                                                                                                                                                                                                                                                                                                                                                      3.43
80.00
40.40%
27.27%
7.30%
                                                                                                                                                                                                                                                                                                              361
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                                                                                                                                                                                                                                                                                                                                                       382 3
673 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
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SEQUENCE
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                                                                               Genew;
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us-09-914-191-1.rsp

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Best Local Similarity:
Query Match:
  1268
1286
1548
1570
2144
                                                                                                        Percent Similarity:
                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
P3K3_DICDI
ID P3K3_DICDI
AC P54675;
 CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      527
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                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                     127
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PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
PROSITE; PS01248; LAMININ_TYPE_BGF; 1
G_protein coupled receptor; Transmembrane; Glycoprotein;
EGF-like domain; Calcium-binding; Laminin BGF-like domain; Repeat;
Developmental protein; Hydroxylation.
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CADHERIN 4.

CADHERIN 4.

CADHERIN 4.

CADHERIN 4.

CACLINE 1.

CACLING BINDING.

EGF-LIKE 2.

CALCIUM-BINDING.

LAMININ G-LIKE 1.

EGF-LIKE 5.

CALCIUM-BINDING.

EGF-LIKE 7.

CALCIUM-BINDING.

EGF-LIKE 7.

CALCIUM-BINDING.

EGF-LIKE 7.

CALCIUM-BINDING.

EGF-LIKE 8.

CALCIUM-BINDING.

EGF-LIKE 9.

CALCIUM-BINDING.

EGF-LIKE 1.

CALCIUM-BINDING.

EGF-LIKE 1.

CALCIUM-BINDING.

EGF-LIKE 1.

CALCIUM-BINDING.

EGF-LIKE 1.

EM SIMILARITY.

BY SIMILA
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CADHERIN 1.
CADHERIN 1.
                                                                                                       2 (POTENTIAL)
EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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491 IleHisProValGlyGlyLeuArgCysArgCysProProGlyPheThrGlyAspTyrCys 510
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  (POTENTIAL).
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01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Phosphatidylinositol 3-kinase 3 (EC 2.7.1.137) (PI3-kinase)
PLOINS-3-kinase) (PI3K) (Fragment)
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570 AsnLeuLeuValGlyGlyPheLysCysAspCysProSerGlyAspPhe
N-LINKED (GLCNAC. ..) (POTI)
N-LINKED (GLCNAC. ..) (POTI)
N-LINKED (GLCNAC. ..) (POTI)
N-LINKED (GLCNAC. ..) (POTI)
MW; 6EA898C1BA655ECA CRC64;
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Eukaryota, Mycetozoa, Dictyostellida, Dictyostellum.
NCBI_TaxID=44689,
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Indels:
Gaps:
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STRAIN-AX3;
MEDLINE=96009592; PubMed=7565716;
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  1268
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AA; 233480 M
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79.50
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391 AAGATGGCAGTGACCCGGACCAGGACAAAGCCAGTGCCCTTGCACTGCGATATCATCGGG 332
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      511 TTCAACATCAACTATAATAATGAGCTGCCGATGTATAGGAAAGGGACTGTGTTGATATGG 452
                                                                                                                                                                                                                                                                                                                                                                                                                               97 AGAACACCTIGITIGGGGIGITIGGAAC------AIGGITICCTITG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTTCAGTTCTGGTGTGCTTAACCATGCAAGCCCTCCCACCTCCCAGGGCTCCTTGCCTT
                                                                                                                                                                                                                                                                                                                                                                   154 GAGGGGAACAGGGAAGGGATGGGATGGGGGGGGGGTGTATCTTACTCTGTTTAAG---C
                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                    TyrAsnLeuAsnTyrAsnAsn-----ProThrGlnLysProThrAsnIle----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 GCAGAAGTGCTT-------TTTTTTTAATCGCAGTACTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=99018217; PubMed=9799833;
MEDLINE=99018217; PubMed=9799833;
MEDLINE, Ambrose H.J., Guay-Woodford L.M., Dasgupta S.,
Nawrotzki R.A., Blake D.J., pavies K.E.;
"Genomic organization and refined mapping of the mouse beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE=98200066; PubMed=9540997;

Muca A.A., Filuso V.N.G., Belsito A., Sampaolo S., Quaderi
Rossi E., Di Iorio G., Ballabio A., Franco B.,

"Identification and characterization of a novel member of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MDTN-B)
                                                                                                                                                      SerLeuGluIleAsnAsnGlyArg-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family.";
Proc. Natl. Acad. Sci. U.S.A. 95:241-246(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=98081858; PubMed=9419360;
Blake D.J., Nawrotzki R., Loh N.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dystrobrevin gene.";
Mamm. Genome 9:857-862(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dystrobrevin gene family.";
FEBS Lett. 425:7-13(1998).
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                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||| |||::::::||||||| ||| || AlaSerGlyLysMetGlnGlyHisLeu 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCCAAGGGAGATTACAGGGAACTCTTNCAGCAGACAAGAATGAGATTTTGTTTTCT---
Zhou K., Takegawa K., Emr S.D., Firtel R.A.;
"A phosphatidylinositol (PI) kinase gene family in Dictyostellium discoideum: biological roles of putative mammalian pl10 and yeast vps34p Pl 3-kinase homologs during growth and development.";
Mol. Cell. Biol. 15:5645-565(1995)
-!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol = ADP 1-phosphatidyl-1D-myo-inositol 3-phosphate.
-!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
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Matches:
Conservative:
Mismatches:
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PROSITE; PS00916; PI3 4 KINASE 2; 1.
PROSITE; PS50290; PI3 4 KINASE 3; 1.
Transferase; Kinase; Multigene family; Repeat.
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InterPro, IPR003420, Pi3K_C2.
InterPro, IPR003420, Pi3K_C2.
InterPro, IPR00341, Pi3K_ras_bind.
InterPro, IPR001263, Pi3Ka.
InterPro, IPR0013, Pi3Ka.
InterPro, IPR0013, Pi3Ka.
Ffam, PF00454, Pi3 Pi4 Kinase, IPR0013, Pi3Ka.
Ffam, PF00792, Pi3K C2, I.
Pfam, PF00792, Pi3K C2, I.
SMART; SM00144, Pi3K rbd, I.
SMART; SM00144, Pi3K rbd, I.
SMART; SM00146, Pi3K rbd, I.
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                                           A Kawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., A Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T., Sakai K., Okido T., Furuno M., Aono H.. Baldarelli R., Barsh G., A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whithaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                 Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
-!- SUBUNIT: INTERACTS WITH DYSTROPHIN SHORT FORM DP71 AND SYNTROPHIN.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- ALTERNATIVE PRODUCTS: AT LEAST Z ISOFORMS; 1 (SHOWN HERE) AND 2;
--- ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: EXPRESSED MAINLY IN BRAIN, KIDNEY, LIVER AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LUNG. IN BRAIN EXPRESSED IN NEURONS OF THE CORTEX AND HIPPOCAMPUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZZ-TYPE.
SYNTROPHIN-BINDING REGION.
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Pfam; PF00569; ZZ; 1
SMART; SM00291; ZnF_ZZ; 1.
PR0SITE; PS50135; ZF_ZZ 1; 1.
PROSITE; PS50135; ZF_ZZ 2; 1.
Colled coll; Zinc-finger; Alternative splicing. 201 RNG 237 284 SYNTROPHIN-BINDING
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 FROM N.A. (ISOFORM 2)
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JOINED.
SEQUENCE OF 590-608 FROM N.A. (ISOF
STRAIN=C57BL/6J; TISSUE=Stomach;
MEDLINE=21085660; PubMed=11217851;
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AJ010204; CAA09038.1;
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                                                                                                                                                                                                                                                    538 GACAAGAATGAGATTTTGTTTTCTGAATTCAACATCAACTATAATAATGAGCTGCCGATG
                                                                                                                                                                                                                                                                                                                                                               418 AAGCTGCCAACAGAAATG---GAAGGAAAAAAGATGGCAGTGACCCGGACCAGGACAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 ATTCTAGATGAAGACAGCTGACCCTTTTGCGCTTCAGTTCTGGTGTGTTAACCATGCAA
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MEDLINE=96254978; PubMed=8845841;
Sadoulet-Puccio H.M., Khurana T.S., Cohen J.B., Kunkel L.M.;
"Cloning and characterization of the human homologue of a dystrophin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DTNA HUMAN STANDARD; PRT; 743 AA. 0294768; 013432; 075697; 0294768; 013499; 013499; 013500; 015332; 075697; 013197; 031998; 015332; 075697; 013197; 013198; 015408; 015409; 015409; 015409; 015409; 016-007-2001 (Rel. 40, Last sequence update) 15-0TN-2002 (Rel. 41, Last annotation update) Dystrobrevin alpha (Dystrobrevin-alpha).
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          K -> KEEECKGA (IN ISOFORM 2).
AEAEEQ -> EVTPVS (IN ISOFORM 2).
MISSING (IN ISOFORM 2).
P -> L (IN REF. 2 AND 3).
S -> F (IN REF. 2 AND 3).
W, 6BE34EE961AFE46C CRC64;
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196 ThrCysPheProGlnGlnLysLysIleMetLeuAsnMetPhe-
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Conservative:
Mismatches:
Indels:
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521 CC
518 K
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412 P
465 S
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Best Local Similarity:
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MISSING (IN ISOFORM 4, ISOFORM 8).
MISSING (IN ISOFORM 4, ISOFORM 6 AND ISOFORM 8).
MISSING (IN ISOFORM 2, ISOFORM 5 AND ISOFORM 8).
PPROSEUR -> DGARGGCV (IN ISOFORM 7).
MISSING (IN ISOFORM 7).
MISSING (IN ISOFORM 6).
TQGAGSPRESPEHTIS -> EBELKQGUSYVPYCRS (ISOFORM 3, ISOFORM 4, ISOFORM 5 AND ISOFORM 3, ISOFORM 4, ISOFORM 5 AND
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E -> Q (IN REF. 1 AND 3).
EVL -> K (IN REF. 3).
EVL -> AVF (IN REF. 1).
E -> K (IN REF. 1).
AG -> GV (IN REF. 1).
AGSP -> SGTH (IN REF. 1; AAC50431).
AGSP -> R (IN REF. 1; AAC50431).
T -> S (IN REF. 1).
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SMART; SW00291; ZnF ZZ; 1.
PROSITE; PS01137; ZE ZZ 1; 1.
PROSITE; PS50135; ZF ZZ 2; 1.
Synapse; Coiled coil; Zinc-finger; Phosphorylation;
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AAB58542.1;
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AAB58541.1;
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DOMAIN 400 450
DOMAIN 461 556
VARSPLIC 335 337
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Genew; HGNC:3057; DTNA.
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                                                                                                                                                                                                                                                ACETYLCHOLINE RECEPPORS.

1. SUBGNIT: INTERACTS WITH DYSTROPHIN, UTROPHIN AND SYNTROPHIN.

1. SUBGNIT: INTERACTS WITH DYSTROPHIN, UTROPHIN AND SYNTROPHIN.

2. SUBGRILLUMAR IOCATION: CY-CPDIAGMIC.

3. SUBCELLUMAR LOCATION: CY-CPDIAGMIC.

4. SUBCELLUMAR LOCATION: CY-CPDIAGMIC.

5. STROBREVIN-ALPHA, 3/DYSTROBREVIN-BETA, 2/DYSTROBREVIN-BETA, 3/DALPHA-DYSTROBREVIN-BETA, 3/DYSTROBREVIN-SEPSILON, 7/DTW-3/ALPHA-DYSTROBREVIN-BETA, 3/DYSTROBREVIN-ESPSILON, 7/DTW-3/ALPHA-DYSTROBREVIN-ESPSILON, 7/DTW-3/ALPHA-DYSTROBREVIN-BETA, 3/DYSTROBREVIN-ESPSILON, 7/DTW-3/ALPHA-DYSTROBREVIN-ESPSILON, 7/DTW-3/ALPHA-DYSTROBREVIN-ESPSILON, 7/DTW-3/ALPHA-DYSTROBREVIN-ESPSILON, 7/DTW-3/ALPHA-DYSTROBREVIN-ESPSILON, 7/DTW-3/ALPHA-DYSTROBREVIN-ESPSILON, 7/DTW-3/ALPHA-DYSTROBREVIN-ESPSILON, 7/DTW-3/ALPHA-DYSTROBREVIN-ESPSILON, 7/DTW-3/ALPHA-DYSTROBREVIN BETA-DYSTROPHIN BY STRIALARITY).

5. DOMAIN: THE COILED-COIL DOMAIN MEDIATE THE INTERACTION WITH DYSTROPHIN BY SIMILARITY).

5. DYSTROBREVIN THE C-TERMINUS (BY SIMILARITY).

5. SIMILARITY: BELONGS TO THE DYSTROPHIN FAMILY. DYSTROBREVIN CHERANTIN
                                                                                                                                                                      related phosphoprotein found at the Torpedo electric organ post-
                                     (2) SEQUENCE FROM N.A. (ISOFORMS 1; 3 AND 7).
SEQUENCE FROM N.A. (ISOFORMS 1; 3 AND 7).
Sadoulet-Puccio H.M., Feener C.A., Schaid D.J., Thibodeau S.N. Michels V.V., Kunkel L.M.;
Michels V.V., Kunkel L.M.;
Withe genomic organization of human dystrobrevin.";
Neurogenetics 1:37-42(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: CONTAINS 1 ZZ-TYPE ZINC FINGER.
             synaptic membrane.";
Hum. Mol. Genet. 5:489-496(1996).
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TISSUE=Fetal brain;
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U26742; AAC50424
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1; AAC50429)

743 23 55 73

Matches: Conservative: Mismatches: Indels:

Length:

us-09-914-191-1.rsp

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                                                                            135 AlaLeuAlaThrLeuCysGlyGlyLysIleMetAspLysLeuArgTyrIlePheSerMet 154
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MEDLINE=9726011; PubMed=9106206;

Mesnage S., Tosi-Couture E., Mock M., Gounon P., Fouet A.;

"Molecular characterization of the Bacillus anthracis main S-layer
component: evidence that it is the major cell-associated antigen.";

Mol. Microbiol. 23:1147-1155 (1997).

-! FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.

-! SUBCELLULAR LOCATION: Cell wall.

-! SIMILARITY: CONTAINS 3 S-LAYER HOMOLOGY (SLH) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus anthracis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 GlnCysHisAsn-TyrGlnLeuCysGlnAspCysPheTrp 272
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-----ProPheGlyAlaAsn-----ThrAlaAlaIleLysGluValLeuProLys-Th
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94140368; PubMed=8307578;
Li X., Pereira L., Zhang H., Sanguineti C., Ramirez F., Bonadio J.,
Li X., Pereira L., Zhang H., Sanguineti C., Ramirez F., Bonadio J.,
"Francke U.;
"Fibrillin genes map to regions of conserved mouse/human synteny on
mouse chromosomes 2 and 18 ";
Genomics 18:667-672(1993)
-!- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS
THAT BINDS CALCIUM. FIBRILLIAN-LONTANING MICROFIBRILS
LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.
-!- SIMILARITY: CONTAINS 7 TGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROTEIN DOMAINS.
            SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=95263670; PubMed=7744963;
Zhang H., Hu W., Ramirez F.;
"Developmental expression of fibrillin genes suggests heterogeneity of extracellular microfibrils.";
"Cell Biol. 129:1165-1176(1995).
"Ronadio J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR001561; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L39790; AAA74908.1; -.
EMBL; S69359; AAC60685.1; -.
HSSP; P35555; 1ENN.
MGD; MGI:95490; Fbn2.
 NCBI_TaxID=10090;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                             Yu W. Gibbs R.A.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-!- SUBUNIT: INTERACTS WITH DYSTROPHIN SHORT FORM DP71 AND SYNTROPHIN.
-!- SUBCELLULAR LOCATION: CYtoplasmic.
-!- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS: 1/PTW-R1 (SHOWN UPDE)
                                                                                                                                                                                                                                                                                                                                                                                                                      -:- SUBCELLULAR LOCATION: CYCOPISENIC.
-:- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS; 1/DTN-B1 (SHOWN HERE), 2/DYSTROPHIN-ASSOCIATED PROTEIN A0, 3/DTN-B2 AND 4; ARE PRODUCED BY ALTERNATIVE SPLICING.
-:- TISSUB SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, KIDNEY AND PANCREAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- DOMAIN: THE COILED-COIL DOMAIN MAY MEDIATE THE INTERACTION WITH DYSTROPHIN.
                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                            TISSUE=Skeletal muscle; when we will muscle; muscle; muscle; pubmed=9540997; when Links=98200066; Pubmed=9540997; Puca A.A., Piluso V.N.G., Belsito A., Sampaolo S., Quaderi N., Rossi E., Di Iorio G., Ballabio A., Franco B.; "Identification and characterization of a novel member of the EBS Lott. appears of the FEBS Lett. 425:7-13(1998).
                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=98058946; PubMed=9395493;
Peters M.F., O'Brien K.F., Sadoulet-Puccio H.M., Kunkel L.M. Adams M.E., Froehner S.C.;
"Beta-dystrobrevin, a new member of the dystrophin family.
Identification, cloning, and protein associations.";
J. Biol. Chem. 272:31561-31569(1997).
       060941; 043782; 060881; 075538; 09UE15; 09UE16; Q9UE14; 16-0CT-2001 (Rel. 40, Last sequence update) 15-0UN-2002 (Rel. 41, Last annotation update) Dystrobrevin beta (Beta-dystrobrevin) (DTN-B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZZ-TYPE.
SYNTROPHIN-BINDING REGION.
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000433; Znf_ZZ.
Pfam; PF00569; ZZ; 1.
PROSTT; SM00291; ZnF_ZZ; 1.
PROSITE; PS50135; ZF_ZZ 1; 1.
PROSITE; PS50135; ZF_ZZ 2; 1.
Coiled coil; Zinc-finger; Alternative splicing.
ZN_FING 237 284 ZZ-TYPE.
ZN_FING 339 448 SYNTROPHIN-BINDING DOMAIN 428 529 COILED COIL (POTEN
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EMBL; Y12712; CAA7349.1; --
EMBL; Y15718; CAA75733.1; --
EMBL; X15719; CAA75734.1; --
EMBL; X15720; CAA75734.1; --
EMBL; X15720; CAA75736.1; --
EMBL; AF670567; AAC28643.1; --
Genew, HGNC:3058; DTNB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF022728; AAC05082.1; -.
 STANDARD;
                                                                                     Homo sapiens (Human)
                                                                                                                         NCBI_TaxID=9606;
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MIM; 602415;
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 CATTCGCACCAGTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTG 230
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AQATGSPHTSPTHGGGRPMPWRSTSAGSTPT -> VSEL
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| 221 CysLeuValTrpLeuProLeuMetHisArgLeuAlaHisValGluAsnValPheHisPro
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RLQYSQDIPSHLADEHALIASYVARLQHCAR -> S (IN
                                                                                                          3).
MISSING (IN ISOFORM 3).
MISSING (IN ISOFORM 2 AND ISOFORM 4);
6927ECOBD86D375C CRC64;
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LysLeuProThrAlaValPheGluGlyProSerPheGlyTyrThr------
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01-DEC-1992 (Rel. 24, Last annotation update)
D-galactose 1-dehydrogenase (EC 1.1.1.48)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dehydrogenase gene.";
Nucleic Acids Res. 17:5402-5402(1989).
-!- CATALYTIC ACTIVITY: D-galactose + NAD(+) = D-galactono-1,4-lactone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=BWTU 102;
MEDLINE=89345117; PubMed=2503815;
Sperka S., Zehelein B., Fiedler S., Fischer S., Sommer R., Buckel P.,
"Complete nucleotide sequence of Pseudomonas fluorescens D-galactose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X14913; CAA33038.1; -.
PIR; S04853; S04853.
InterPro; IPR000683; GFO_IDH_MOCA..
InterPro; IPR000683; GFO_IDH_MOCA_C.
Pfam; PF01408; GFO_IDH_MOCA, 1.
Pfam; PF02844; GFO_IDH_MOCA, 2.
Oxidoreductase; NB, Galactose metabolism.
SEQUENCE 304 AA; 33049 MW; D842A776DC67A3B0 CRC64;
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                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Cytoplasmic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

STRAIN-BALB/C; TISSUE-SKeletal muscle;
MEDLINE-98340858; PubMed=9675094;
A Takahashi H., Noda S., Imamura Y., Nagasawa A., Kubota R., Mashima Y.,
A Kudoh J., Oguchi Y., Shimizu N.;
Mouse myocilin (Myoc) gene expression in ocular tissues.";
Mouse myocilin (Myoc) gene expression in ocular tissues.";
Biochem. Biophys. Res. Commun. 248:104-109(1998).

THE TRABECULAR MESHWORK.

THE TRABECULAR LOCATION: LOCATED PREFERENTIALLY IN THE CILIARY
ROOTLET AND BASAL BODY OF THE CONNECTING CILIUM OF PHOTORECEPTOR
CELLS. AND IN THE ROUGH ENDOPLASMIC RESTICULUM. ALSO SECRETED.

TISSUE SPECIFICITY: EXPRESSED IN CILIARY BODY. IRIS, RETINA,
TRABECULAR NETWORK AND SCIERA BUT NOT IN LENS OR CORNEA. ALSO
EXPRESSED STRONGLY IN SKELETAL MUSCLE AND WEAKLY IN HEART, BRAIN,
TESTIS, LIVER, KIDNEY, THYROID AND EPIDDYMIS. NO EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98217378; PubMed=9548973; Fingert J.H., Ying L., Swiderski R.E., Nystuen A.M., Arbour N.C., Alward W.L.M., Sheffield V.C., Stone E.M.; "Characterization and comparison of the human and mouse GLCIA glaucoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLYMORPHISM: VARIANT ALA-164 IS FOUND IN STRAIN BALB/CJ WHICH HAS A LOW INTRACCULAR PRESSURE. VARIANT THR-164 IS FOUND IN STRAINS C3H/HBJ AND C57BL/6J, TWO STRAINS WHICH HAVE A RELATIVELY HIGH INTRACCULAR PRESSURE.
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metzoza; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND VARIANT ALA-164.
STRAIN=BALB/CJ, C3H/HeJ, and C57BL/6J; TISSUE=Brain, and Muscle;
MEDLINE=98249809; PubMed=9588210;
TOMATCA S.I., Tamm E.R., Chang B. Myoc/Tigr gene.";
"Characterization of the mouse Myoc/Tigr gene.";
Biochem. Biophys. Res. Commun. 245:887-893(1998).
                                                                                                                                                                          070624; 070289;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Myocilin precursor (Trabecular meshwork-induced glucocorticoid response protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
.
MEDLINE=98345432; PubMed=9680392;
Abderrahim H., Jaramillo-Babb V.L., Zhou Z., Vollrath
"Characterization of the murine TIGR/myocilin gene.";
mmm. Genome 9:673-675(1998).
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                                                                                                                                                          490 AA
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EMBL; AF041333; AAC32805.1; JOINED.
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                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=129/Sv;
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                                                                                                                                                       MOUSE
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469 GGGACTGTGTTGATATGGCAGAAGGTGGATGAAGTGATGACAAAAGAAATTAAGCTGCCA 410
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145 LeugluGlnGluAsnGluAspLeuAlaArgArgLeuGluSerSerGluGluValThr 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 ArgLeuArg-ArgGlyGlnCysProSerThrGlnTyrProSerGlnAspMetLeuProGl 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262 GIGIGCITAACCATGCAAGCCCTCCCACCTCCCAGGGCTCCTTGCCTTAGGTGGCTGTAG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 CATCCCTACCACCCAGGACACTGGTGCGAATGACACAACTCAAGTTGGGAGGGGAACAGG 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluthrGlnthrArgAspLeuGluAlaAlaTyrAsnAsnLeuLeuArg------
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                                                                                                                                                                                                                                     OLFACTOMEDIN-LIKE.

N-LINKED (GLCNAC. ) (POTENTIAL)

T -> A (IN STRAIN BALB/CJ).

2F090571E97B0425 CRC64;
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449
114
63
63
                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                    Coiled coil, Glycoprotein, Signal, Polymorphism.
SIGNAL 1 18 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1570 AA
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          EMBL, AF049796, AAC14265.1;
EMBL, AF049795, AAC14265.1;
EMBL, AF049794, AAC14265.1; JOINED.
EMBL, AF039869, AAC40112.1;
EMBL, AB013592; BAA32031.1;
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                                                                                                  MGD; MGI:1202864; Myoc.
InterPro; IPRO03112; Olfac_like.
Pfam; PF02191; OLF; 1.
SMART; SM00284; OLF; 1.
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164 T
55314 MW;
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76.00
33.87
26.34
6.88
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                                                                                                                                                                                                                                                                                         490 AA;
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Best Local Similarity:
AF041334; AF049796;
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232
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164
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P3K1 DICDI
ID P3K1 DICDI
AC P54673;
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SEQUENCE
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DB:
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508 AACATCAACTATAATAATGAGCTGCCGATGTATAGGAAAAGGGACTGTGTTGATATGGCAG 449

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                                                                                                                                                                                                                    Zhou K., Takegawa K., Emr S.D., Firtel R.A.;
"A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoideum: biological roles of putative mammalian pil0 and yeast vps34p PI 3-kinase homologs during growth and development.";
Mol. Cell. Biol. 15:5645-5656(1995).
-!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol = ADP
Ol-OCT-1996 (Rel. 34, Created)
Ol-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Phospharidylinosicol 3-kinase 1 (EC 2.7.1.137) (PI3-kinase)
PIKA OR PIKI.
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W; 55B678B72B34D783 CRC64;
                                                                                                                                                                                                                                                                                                                  1-phosphatidyl-1D-myo-inositol 3-phosphate.
-!- SIMILARITY: BELONGS TO THE P13/P14-KINASES FAMILY.
                                                                                                               Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBL_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (or send an email to license@isb-sib.ch)
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POLY-ASN.
POLY-ASN.
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POLY-ASN
POLY-THR
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nterPro; IPR000403; PI3 PI4 kinase.
nterPro; IPR000605; Ubiquitin.
fam; PF00240; ubiquitin; 1
fam; PF00454; PI3 PI4 kinase; 1.
fam; PF00613; PI3Ka; 1.
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InterPro; IPR002420; PI3K_C2.
InterPro; IPR000341; PI3K_ras_bind.
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PROSITE; PS00916; PI3 4 KINASE 2;
PROSITE; PS50290; PI3 4 KINASE 3;
                                                                                                                                                                                                         MEDLINE=96009592; PubMed=7565716;
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Pfam; PF00794; PI3K_rbd; 1.
SMART; SM00142; PI3K_rbd; 1.
SMART; SM00144; PI3K_rbd; 1.
SMART; SM00145; PI3Ka; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U23476; AAA85721.1; -.
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1570 32 12 27 54

Length:
Matches:
Conservative:
Mismatches:
Indels:

10.2 76.00 35.20% 25.60% 6.88%

Best Local Similarity: Percent Similarity

Query Match:

Alignment Scores:

. No. .

US-09-914-191-1 (1-598) x P3K1_DICDI (1-1570)

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842 GInileThrHisileSerileArgGluileLysELysProPheArgVal-----LysVal 859
ATGGCAGTGACCCGGACCAGGACCAGTGCCTTGCACTGCGATATCATCGGGGAT 329
                                                                                                 869
                                                                                                                                                               877
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878 VallleValSerIleSerLeuTyrHisGlyIleGluCysPheSerLysAlaPheThrGln 897
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                                                                                                                                GCTTTCTGGAAGGAACATCCAGAGATTCTAGATGAAGACAGCTGACCCTTTTTGCGCTTCA
                                                                                                                                                                  --SerSer
                                                                                               860 MetGlySerThrArg------IleProLeuSerCys-----
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Job time : 22 secs
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Q9V318 drosophila
Q9V713 schizosacch
Q9X713 schizosacch
Q9X615 arabidopsis
Q91215 arabidopsis
Q918215 arabidopsis
Q91827 bombyx mori
Q91979 arabidopsis
Q91071 homo sapien
Q22742 arabidopsis
Q917C8 arabidopsis
Q917C8 arabidopsis
Q917C8 arabidopsis
Q957C8 bombyx mori
Q8VSZ6 nabaena sp
Q9C019 homo sapien
Q9C019 homo sapien
Q9C019 homo sapien
Q9C114 pichia past
Q9TD2 rattus norv
Q9AVE cenorhabdi
Q9M72 rattus norv
Q9AVE methanopyru
Q9Wv0 rattus norv
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Q12393 saccharomyc
Q60021 thermus aqu
Q9fgw5 arabidopsis
Q85735 murine type
Q9c2a4 neurospora
                                      Q9cqt0 mus musculu
Q9cy52 mus musculu
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Q94hv6 oryza sativ
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ13293 fis, clone OVARC1001188 (Similar to hypothetical protein
FLJ20546) (Hypothetical 20.2 kDa protein)
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
  29h0s2
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09Y7T3
09SIQ0
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Q9NS06
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09FYC8
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089276
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Q8TZ46
Q9WVH4
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  Homo sapiens (Human)
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TISSUE=OVARY;
NCBI_TaxID=9606;
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169.5
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DT 01-D
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-MODEL=frame+ n2p-model -DEV=x1p
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-MODEL=frame+ n2p-model -DEV=x1p
-Q=/Cgn2 1/USFO_spool/US09914191/runat_09072003 112349_12876/app_query.fasta_1.775
-DB=SFPREMBL_21 -QFMT=fastan -SURFIX=rspt -MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -STAXT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -STAXT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -STAXT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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                                                                                                                                     July 9, 2003, 12:45:58; Search time 47.5 Seconds
                    GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                              - protein search, using frame_plus_n2p model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
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sp_bacteria:*
sp_fungl::*
sp_human:*
sp_invertebrate:*
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Similarity:
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                   Strausberg R.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO2335; BAB14540.1;
EMBL; BCO01852; AAH01652.1;
EMBL; BCO01523; AAH01523.1;
                                                                             to the EMBL/GenBank/DDBJ databases
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 34.8 kDa protein.
DKF2P564B1172.
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Matches:
Conservative:
Mismatches:
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SEQUENCE 173 AA; 20157 MW;
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99.04%
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                                                                           Submitted (JAN-2001)
                                                                                                               SEQUENCE FROM N.A.
TISSUE=MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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                                       TISSUE=MUSCLE;
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Pred. No.:
                                                         Strausberg R
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"NEDO human cDNA sequencing project.";

Submitted (Aug-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AK001653; BAB13870.1;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
"NEDO human CDNA sequencing project.",
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
Analysis of 500 Novel Complete Protein Coding Human cDNAs."; Genome Res. 11:422-435 (2001).

EMBL; AL136669; CAB66604.1; -.

Hypothetical protein.

SEQUENCE 298 AA; 34831 MW; A6C941B75611C448 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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TISSUE=EMBRYO;
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Percent Similarity:
Best Local Similarity:
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                                                                         Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                              LysLeuProThrGluMetGluGlyLysLysMetAlaValThrArgThrLysPro
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
AA; 34815 MW; A6C951E716019408 CRC64;
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Last sequence update)
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Matches:
Conservative:
Mismatches:
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MEDLINE=21085660; PubMed=11217851;
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5730409G07RIK.
Mus musculus (Mouse).
                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
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 298
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SEQUENCE FROWN N.A.

KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radca K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radca K., Matsuda Y., Nikaido I., Pesole G., Quackenbush J.,

Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Baka J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGCTGCCAACAGAAATGGAAGGAAAAAAAGATGGCAGTGACCCGGACCAGGACAAAGCCA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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EMBL; AKO16076; BAB30104.1; -.
EMBL; AKO15467; BAB29859.1; -.
EMBL; AKO13467; BAB298607R; SEQUENCE 238 AA; 27998 MW; SEQUENCE
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5730409G07RIK.
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SEQUENCE 28
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Richards S.A., Ashburner M., Henderson S.N.,
A. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
B. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
B. Brandon R.C., Rogers Y.-H.C., Blazelj R.G., Champpe M., Pfelifer B.D.,
M. M. K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
B. Belson K.Y., Benos P.V. Berman B.P., Bhandari D., Bolshakov S.,
B. Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brottier P.,
B. Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
A. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A. Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 16, Last annotation update)
61-MAR-2001 (TrEMBLrel. 16, Last annotation update)
62-MAR-2001 (TrEMBLrel. 16, Last annotation update)
63-MAR-200929-4 Protein.
63-MAR-200929-4 OR C4103-7
63-MAR-2004-1 MAR-2004-1 Protein Hexapoda; Insecta;
64-MAR-2004-1 Protein Hexapoda; Tracheata; Hexapoda; Insecta;
65-MAR-2004-1 Protein Hexapoda; Diptera; Brachycera; Muscomorpha;
67-MAR-2004-1 Protein Hexapoda; Diptera; Brachycera; Marcomorpha;
67-MAR-2004-1 Protein Hexapoda; Diptera; Protein H
Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK010876; BAB27240.1; -.
MGD; MGI:1913878; 5730409G07Rik.
SEQUENCE 298 AA; 34971 MW; D4CAOC154E452ECA CRC64;
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Matches:
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535 AAGAATGAGATTTTGTTTTCTGAATTCAACATCAACTATAATAATGAGCTGCCGATGTAT 476
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Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Calodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris M., Harris M., Hauvey D., Heiman T.J., Mei M.-H., Ibegwam C., Analain M., Kalubak F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Karfet C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPharson D., Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reses M.G., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Shen H., Anelson K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Sidelling A.C., Stapleron M., Strong R., Sun E., Spier E., Spradling A.C., Stapleron M., Strong R., Sun E., Shing M., Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Welliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Welliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhao Q., Zheng T., The genome sequence of Drosophila melanogaster.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T., Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D., Hong L., Houston K., Hokins R., Johnson G., Martin C., Moshrefi A., Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw P. Celniker S., Rubin G.M.;

"An exploration of the sequence of a 2.9-Mb region of the genome of Genetics 153:179-219(1999).
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286 Aa; 33072 MW; 9539693DA9C2BFC8 CRC64;
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Matches:
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FlyBase; FBgn0028925; BG:DS00929.4.
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LysSerGlyLysSerValSerGluThrGlnGlulleLeuLysAspThrGlnLysGlnGln 185
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Eukaryota, Viridiplantae; Srreptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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LysAsnGluLeuLeuPheGlnLysPheGlyIleAsnTyrLysThrLeuProGluLeuPhe
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|ArgGlnGlySerCysLeuPheLysLysLysValGluGluThrVal-------
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                      STRAIN-CV. COLUMBIA;
Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., Vanaken S.E.,
Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., Vanaken S.E.,
Barnstead M.E., Mascon T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
Fraser C.M., Venter J.C.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AC007071; AAD24854.2;
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9
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    01-MAY-2000 (TrEMBLrel. 13, Cro
01-JUN-2002 (TrEMBLrel. 21, Las
01-JUN-2002 (TrEMBLrel. 21, Las
Hypothetical 57.9 kDa protein.
                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 495 AA; 57942 MW;
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129.50
51.96%
31.37%
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Murphy L., Harris D., Wood V., Rajandream M.A., Barrell Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases. - I- SIMILARITY: TO YEAST YGR024¢. EMBL, AL049522; CAB40011.1; -. Hypothetical protein.
                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Hypotherical 31.1 kDa protein C63.07 in chromosome III.
SPCC63.07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al protein.
261 AA; 31063 MW; FCC4B047C3D2D7DA CRC64;
                                                                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
Bukarycta; Fungl; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
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------IleLeuGlyGluLys-----
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169.50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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Ever J.R.;
Ever J.R.;
"Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AYO56804; AA110495.1;
ThterPro; IPR003851; Znf_Dof.
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SEQUENCE 297 AA; 34814 MW; E7581E66D57A7DA3 CRC64;
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                                                                                                                                                                                                                                                                                                            US-09-914-191-1 (1-598) x Q9ZV61 (1-297)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                               0.129
94.00
62.75%
39.22%
8.51%
                                                                                                                 Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                      Percent Similarity
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                                                                                                       thaliana
                                                                                                                                                             Lin X.;
                                                                                                                                                                                                                                                                           Query Match:
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Length:

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232
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267 ValProLeuAsnGlnThrAsnGluGluAlaArgThrVal-----SerProLeuProLys 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 AGGTGGGAGGGCTTGCATGGTTAAGCACACCAGAACTGAAGCGCAAAAGGGTCAGCTGTC 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 GTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACCACCCCCATCC 130
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                                                                                                                                                                                 71 GTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACCACCCCCATCC.
                                                                                                                                                                                                                                                                                                   :::
||||||||||
305 ThrIleLeuProPheTyrProProPlaTyrTrpSerCysProGlyValSerProGly
                                                                                                                                                                                                                                                                                                                                                                   ----AGCCCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 ValProLeuAsnGlnThrAsnGluGluAlaGlyThrVal-----SerProLeuProLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 ATCCCTTCCCTCCCTGTTCCCCTCCCAACTTGAGTTGTGTCATTCGCACCAGTGTCCTGG
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98401884; PubMed-9734815;
Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structural analysis of Arabidopsis thaliana chromosome 5. VI. Sequence features of the regions of 1,367,185 bp covered by 19 physically assigned Pl and TAC clones.";
DNA Res. 5:203-216(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E2B5BF1957DC33FF CRC64,
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28
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  332 33
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
11-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Similarity to H-protein promoter binding factor.
Arabidopsis thaliana (Mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                337
                                                                                                                                                                                                                                                                                                                                                              191 GTGGTAGGGATGCTACAGCCACCTAAGGCAAGG----
                     Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 TICATCIAGAAICICIGGAIGIICCITCCAGAAAGC
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Indels:
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Matches:
                                                                       Indels:
                                                                                                                                    x Q93ZL5 (1-457)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      325 AlaTrpAsnSerPhe-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AB012243, BAB08898.1; ...
InterPro, IPR003881, Znf. Dof.
Pfam, PF02701, zf.-Dof, 1.
SEQUENCE 515 AA; 5658 MW;
88.50
35.87%
30.43%
8.07%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.569
88.50
35.87%
30.43%
8.07%
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                                                                                                                                US-09-914-191-1 (1-598)
                Percent Similarity:
Best Local Similarity:
Query Match:
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|GInArgLeuLeuAlaSerAlaLeuGlnIleHisArgPheHisProCysTrpProLysGly 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 ACTGAAGCGCAAAAGGGTCAGCTGTTTCATCT-----AGAATCTCTGGATGTTCCTTC 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321 CAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTGGCTTTGTCCTGGTCCGGGTC 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            381 ACTGCCATCTTTTTCCTTCCATTTCTGTTGGCAGCTTAATTTCTTTTGTCATCACTTCA 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCACCTTCTGCCATATCAACACAGTCCCTTTCCTATACATCGGCAGCTCATTATAG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuProValGlyThrLeuLysGlnLeuGlu-----AspAlaThrGluThrThrCysAsn 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::: :::|||::: |||
270 TyrSerThrGlnValLeuLeuArgGluValTyrGlnSerPro-------CysThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 AGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGAGGGCTTGCATGGTTAAGCACACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 AsnAlaAlaLeuCysArgAspLeuValSerGlyLeuPheAsnIleSerSerCysProPhe
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                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                 to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                     495 AA; 54319 MW; A76468A0CBF86AAC CRC64;
                                                                                                                                                                                                                                                                                                                                                              4495
20 20
33 33
               01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Ectonucleoside triphosphate diphosphohydrolase 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
                                                                                                                                                                                 Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ
EMBL; BC011241.1; -.
MGD; MG1:1096863; Entpd2.
InterPro; IPR000407; GDAl_CD39_NTPase.
Pfam; PF01150; GDAl_CD39; 1.
PROSITE; PS01238; GDAl_CD39_NTPASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches:
Indels:
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 Created)
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Q9LP79;
01-OCT-2000 (TEMBLrel. 15,
01-OCT-2000 (TEMBLrel. 15,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                    1.59
84.50
37.80%
25.61%
7.71%
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                                                                                 Mus musculus (Mouse)
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                        Hydrolase.
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AC Q9
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305 ThrileLeuProPheTyrProProPlaTyrTrpSerCysProGlyValSerProGly 324
                                                                                AGGTGGGAGGCTTGCATGGTTAAGCACACCAGAACTGAAGCGCAAAAGGGTCAGCTGTC 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :::::::::||| :::
136 IleGluSerGluGlyGluMetAsnAspThrProGlnAspAspGluAlaGluLysLysAsp 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346 TGCGATATCATCGGGGATGCTTTCTGGAAGGAACATCCAGAGATTCTAGATGAAGACAGC 287
                   ---AGCCCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTACAAGCCCAAGGGAGATTACAGGGAACTCTTNCAGCAGACAAGAATGAGATTTTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hagiwara K., Tomita M., Kobayashi J., Miyajima S., Yoshimura T.;
"Nucleotide sequences of Bombyx mori cytoplasmic polyhedrosis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    segment 8.";
Biochem. Biophys. Res. Commun. 247:549-553(1998).
EMBL; ABO16437; BAA32043.1; -.
SEQUENCE 390 AA; 44151 MW; B172F1D7E790E2B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          390
27
24
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43
                                                                                                                                                                                                                                                                                 (TrEMBLrel. 08, Created)
(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                 Bombyx mori cytoplasmic polyhedrosis virus (BmCPV).
Viruses; dsRNA viruses; Reoviridae; Cypovirus.
VCBI_TaxID=31594;
                                                                                                                                                  TTCATCTAGAATCTCTGGATGTTCCTTCCAGAAAGC 328
                                                                                                                                                                                   ------ThrTrpMetProGlnProAsnSer 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                 191 GTGGTAGGGATGCTACAGCCACCTAAGGCAAGG--
                                                                                                                                                                                                                                                     390 AA
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                                                                                                                 325 AlaTrpAsnSerPhe-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98321164; PubMed=9657006;
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85.00
50.00%
26.47%
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                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel
Non-structual protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 TGACCC 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
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01-NOV-1998
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Q921R1;
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DB:
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                                                                                                                                                                                                                    RESULT 12
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Pfam; PF00096; zf-C2H2; 2.
SMART; SM000355; ZnF C2H2; 2.
PROSITE; PS00028; ZINC FINGER C2H2 1; 1.
PROSITE; PS50157; ZINC FINGER C2H2 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-binding; Metal-binding; Zinc-finger.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 10,-UTN-2002 (TrEMBLrel. 21, 1) KIAA1555 protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 TTAAGCACACACAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTAGAATCTCTGGAT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 LysSerGlySerValSerPheAsnGlyLeuThrHisGlnLeuValGluGluSerLysLeu 108
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Cheuk K., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
Lee J., Lenz C., Lid J., Liu A., Liu J., Liu S., Mukharsky N.,
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
Thaologis A., Ecker J.,
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 SerLysAlalleCysLeuGlyPheLeuProProArgLeuArgPheSerSerProArgLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 CCCTTCCTTCCCTGTTCCCCTCCCAACTTGAGTTGTGTCATTCGCACCAGTGTCTGGGT
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                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Chao O., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J.,
Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
Toriumi M., Vaysberg M., Yu G., Pederspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genomic sequence for Arabidopsis thaliana BAC T1N15 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the EMBL/GenBank/DDBJ databases
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01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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                                                         Arabidopsis thaliana (Mouse-ear cress)
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Submitted (JAN-2000)
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Best Local Similarity:
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1204 LeuAlaArgLysHisSerLeuThrLysAsnAsp---SerSerProGln---ArgCysSer 1221
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                                                                                                   LysAsnAspThrValAlaGlyArgSerGluIleValThrSerPheCysPheGluThrVal 168
                                                                                                                                                                      ---CAGTCCCTT 471
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MEDLINES-20450683; PubMed=10997877;

MEDLINES-20450683; PubMed=10997877;

Magase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.;

"Prediction of the coding sequences of unidentified human genes.

"XVIII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";

DNA Res. 7:273-281(2000).
109 ValSerAlaProPheGlnGluGluLysGlySerPheLeuTrpValLeuAlaProValVal
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                                                          CTGCCATCTTTTTCCTTCCATTTCTGTTGGCAGCTTAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                    472 TCCTATACATCGCCAGCTCATTATTAGT 501
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1262 CysProLeuGlyArgGluLeuAlaProArgAlaHisValLeuSerLysLeuGluGlyThr 1281	TGGGTGGTAGGATGCTACAG 208	::: INTASPPTOGIYLEUPTOATGTYTSETPTOThTATGATGTTPSETPTOGIYGINAlaGIU 1301	TAAGGCAAGGAGCCCTGGGAGGTGGAGGGCTTGCATGGTTAAGCACACCAG 265		SCGCAAAAGGGTCAGCTGTCTTCATCTAGAATCTCTGGATGTTCCTTCGAGAA 325	:::	326 AGCATCCCCGATGATATCGCAGTGCAAGGCACTGGCTTTGT 367		382		TGCCARCTTTTTCCTTCCATTTCTGTTGGCAGCTTAATTTCTTTGT 430		431 CATCACTICATCCACCTICTGCCATATCAACACAGTCCCTTTCCTATA 478	
CysProLeuGly		ThrAspProGly	CCACCTAAC	SerProProArg	AACTGAAGCGC	::: SerAlaGlyGlu	AGCATCCCCGA1	FroLeuProHis		GluSerArgSer	TGCCA1	 SerAlaLeuHis	CATCACTICATO	
1262	188	1282	209	1302	266	1321	326	1341.	368	1361	383	1381	431	1401
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Search completed: July 9, 2003, 12:50:28 Job time: 53.5 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

July 12, 2003, 13:00:53 ; Search time 1245 Seconds (without alignments) 13978.697 Million cell updates/sec Run on:

US-09-914-191-1 598 Title: Perfect score:

1 ttggaatagttcttgcttta......ggtgttagtccagattgttg 598 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

2054640 seqs, 14551402878 residues Searched:

Total number of hits satisfying chosen parameters:

4109280

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

GenEmbl: *

1: gb ba: *

2: gb_htg: *

2: gb_on: *

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em_htg_other:* em_htg_mus:* em_htg_mus:* em_htg_pln:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sullivar, D 09/91419

SUMMARIES

	Description		339 Sedne	523 Homo	2 Ношо	553 Homo	0953 Homo	0moH 699	663 Ношо	55 Homo	407 Homo	186 Homo	90 SHGC-5834	SHGC-5	8 Mouse D			S.pombe	_	38 Drosophi	Drosophi	11 Drosophi	Seguen	C020869 Mus musc	39 S.cerev	n,	Oryza		Strong	Rat		Mus	Mou		Ношо	Homo	179 Ношо вар	0022 Genom	5735 Homo	3560 Homo sa	5064 Rattu	5338	1386	5390	0737	AJ314911 Dictyoste	16425 Dictiost	
SUMMARIES	ID	1 6	5	BC001523	35	S	53	HSM801637	AK021663	S	AC026407	HUMZD93F03	G38490	G3734	AL6459	₹*	45	SPCC63	AC019777	23	AE003646	DROSADH05		σ	22	AF429315	AC097111	AC097112	AC131508	AC120699	AC117082	AC102661	AL646042	AC084019	370	AC023437	17	α,	m	356	ø	n	œ	163	7375	DDI314911	42	
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ALIGNMENTS

PAT 22-SEP-2000 linear DNA Sequence 1 from Patent WO0050637. AX034339 AX034339.1 GI:10303095 human. RESULT 1
AX034339
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
CEYWORDS
SOUNCE
ORGANISM

Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 598)
Godson, C.M., Brady, H.R. and Martin, F.M.
Identification of genes having a role in the presentation of diabetic nephropathy

REFERENCE AUTHORS TITLE

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FWKEHPEILDEDS"
                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 3 Row: b Column: 4.

Location/Qualifiers
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Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadam@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
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                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue type="Muscle, rhabdomyosarcoma"
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                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
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/organism="Homo sapiens"
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                          NIH-MGC Project URL: hi
Contact: MGC help desk
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Matches 597; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1208)

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Direct Submission
Submitted (21-DEC-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Patent: WO 0050637-A 1 31-AUG-2000;
GODSON CATHERINE MARY (IE) ; BRADY HUGH REDMOND (IE) ; HIBERGEN
LIMITED (IE) ; MARTIN FINIAN MARY (IE) ; UNIV COLLEGE DUBLIN
NATIONAL U (IE)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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AUTHORS
TITLE
JOURNAL
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481 TCGGCAGCTCATTATTATAGTTGATTTCAGAAAACAAAATCTCTTTTTTTT	JOURNAL Submitted (129-JAN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room ilA03, Bethesda, MD 20892-2590, USA REMARK VIH-MGC Project URL: http://mgc.nci.nih.gov CONTACT: Gagabb-refmail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org contact: amadan@systemsbiology.org Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia Greene, Mark Ketteman and Anuradha Madan Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Libra at: http://image.llnl.gov	rce	PASE COUNT 346 a 258 c 315 g 289 t ORIGIN Query Match Best Local Similarity 99.8%; Score 597; DB 9; Length 1208; Best Local Similarity 99.8%; Pred. No. 2.76-160; Matches 597; Conservative 0; Mismatches 1; Indels 0; Gaps 0; QY 1 TTGGAATAGTTCTTGCTTTATAAAATAGTACTGCGATTAAAAAAAA

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Direct Submission
Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,
Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 153-23 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NBDO human cDNA sequencing project supported by Ministry of
Enternational Trade and Industry of Japan; CDNA full insert
sequencing: Research Association for Biotechnology; CDNA library
construction, 5' & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Nabekura, T., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y. and Oshima, A. NBO, human cDNA sequencing project
                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.3e-158;
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/note="cloning vector: pME18SFL3"
463 c 522 g 567 t
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  clone_lib:HEMBAl clone:HEMBA1002267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                location/Qualifiers
                                                                                                                                                                                                                                                        (bases 1 to 2159)
[sogai, T. and Otsuki, T.
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Best Local Similarity 99.3%;
Matches 593; Conservative
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TITLE
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LHCDIIGDAFWKEHPEILDEDS"
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2159 bp mRNA linear PRI 01-AUG-2002 Homo sapiens cDNA FLJ10091 fis, clone HEMBA1002267; weakly similar construction accordin mRNA.
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oligo capping; fis (full insert sequence).
Homo sapiens embryo, 10 weeks whole embryo, mainly head cDNA to
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 593.8; DB 9;
Pred. No. 2.2e-159;
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ORIGIN Query Match Query Match Best Local Similarity 99.2%; Pred. No. 1.9e-158; Matches 593; Conservative 0; Mismatches 5; Indels 0; Gaps 0; Qy 1 TTGGAATGTTCTTGCTTTATAAAATAGTACTGCGATTAAAAAAAA	Qy 61 AAGGAACCATGTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACC 120 Db 1140 AAGGAACCATGTTCCAACACGCAAACAAGGTTTCTGCTTAAACAGAGTAACATCC 1081 Qy 121 ACCCCCATCCATCCTTCCTTCCCTTCCCTCCCCCCCAACTTGAGTTGTCATTCGCACC 1081 Db 1080 ACCCCCATCCATCCTTCCTTCCTTCCCTGTCCCTCCCAACTTGAGTTGTCATTCGCACC 1021 Qy 181 AGTGTCCTGGGTGGTACAGCACTCCCTCCCAACTTGAGTTGTCATTGGCACC 1021 Db 1020 AGTGTCCTGGGTGGTACAGCACCCTAAGGCAAGGAGCCCTGGGAGGTGGGA 961 Qy 241 GGGCTTGCATGGGTGGTACAGCACCCTAAGGCAAGAGCCCTGGGAGGTGGGA 961 Qy 241 GGGCTTGCATGGTTAAGCACACCAGAACTGAAGGGCAAAAGGACCCTGGGAGTGGGA 961 Db 960 GGGCTTGCATGGTTAAGCACACCAGAACTGAAGCGCAAAAAGGGTCAGCTGTTCATCTA 901	Qy 301 GARICTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGCACTG 360 Db 900 GAATCTCTGGATGTTCCTTCCAGAAGCATCCCCGATGATTCGCAGGCACTG 841 C 361 GCTTTGTCCTGGATCACTCCCCCATTTTTTTCCTTCCATTTCTTGTTGGCACTGCATA 420 B40 GCTTTGTCCTGGTCCAGGTCACTCCTTTTTTTCCTTCCATTTCTTTGTTGGCAGCTTAA 781 C 21 TTTCTTTTGTCATCATCACTCATCTTTTTTCCTTCCATTTCTTTGTTGGCAGCTTAA 781 C 481 TCGGCAGCTCATTATATATATAGTTGAAATCAACAAAATCTCCTATACA 721 Qy 481 TCGGCAGCTCATTATATATAGTTGATGTTGAAAAAAAAATCTCTTGTTGTCG 540 C 1 CTGGAAGGTCATTATTATAGTTGATGTTGAAATCAGAAAAATCTCATTCTTGTCG 661 Qy 541 CTGAAAAAGGTTCCCTGTAATTGATGTTGAAATCAGAAAAATCTCTTTGTCTG 540 C 1 CTGGAAGGTTCCTTTATTATATAGTTGATGTTGAAAAAAAA	RESULT 7 AK021663 LOCUS LOCUS LOCUS DEFINITION Homo sapiens CDNA FLJ11601 fis, clone HEMBA1003893. ACCESSION AK021663. AK021663. AK021663. GI:10432893 AK021663.1 GI:10432893 AK021663.1 GI:10432893 AK021663.1 GI:10432893 AK021663.1 GI:10432893 AK021663.1 GI:10432893 AK021663.1 GI:10432893 CRGANISM Homo sapiens embryo, 10 weeks whole embryo, mainly head CDNA to mRNA, clone lib:HEMBA1003893. ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE AUTHORS Nishikawa,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Wagatsuma,M., Takahashi,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Sugawara,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Magahari,K., Yamamoto,J., Wakamatsu,A., Ishida,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nakamira,Y., Sugai,T. Indulished Unpublished Unp
482 CGGCAGCTCATTATTATAGTTGATGTTGAATTCAGAAAACAAAATCTCATTCTTGTCTGC 541 1307 CGGCGGCTCATTATTATAGTTGATGTTGAATTCAGAAACAAAATCTCATTCTTGTCTGC 1248 542 TGNAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTACTGGCTGTTAGTCCAGATTGTTG 598	RESULT 6 HSM801637 LOCUS LOCUS LOCUS DEFINITION Homo sapiens mRNA; CDNA DKFZp564B1172 (from clone DKFZp564B1172); complete cds. ACCESSION AL13669.1 GI:12052861 REYWORDS SOURCE Human. ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases I to 1218. AUTHORS Wiemann, S., Weil, B., Wellenreuther, R., Gassenhuber, J., Glassl, S., Ansorge, W., Boecher, M.; Bloecker, H., Bauersachs, S., Blum, H., Lauber, J., Duesterhoeft, A., Beyer, A., Koehrer, K., Strack, N., Mander H. Duesterhoeft, A., Beyer, A., Tampa, J. Hambar, H., Mander H. Duesterhoeft, A., Beyer, A., Tampa, J. Hambar, H., Mander H. Duesterhoeft, A., Beyer, A., Tampa, J. Hambar, H., Mander H. M. Ortennasalor B. Tampa, J. Hambar, H., Mander H. M. Ortennasalor B. Tampa, J. Hambar, H., Mander H. M. Ortennasalor B. Tampa, J. Hambar, H., Mander H. M. Ortennasalor B. Tampa, J. Hambar, H., Mander H. M. Ortennasalor B. Tampa, J. Hambar, H., Mander H. M. Ortennasalor B. Tampa, J. Hambar, H., Mander H. M. Ortennasalor B. Tampa, J. Hambar, H., Mander H. M. Ortennasalor B. Tampa, J. Hambar, H., Mander H. M. Ortennasalor B. Mander B. Tampa, J. Hambar, H., Mander H. M. Ortennasalor B. Mander B. Tampa, J. Hambar, H., Mander H. M. Ortennasalor B. Mander B. Tampa, H., Mander H. M. Ortennasalor B. Mander B. Tampa, H., Mander H. M. Ortennasalor B. Mander B. Tampa, H., Mander H. M. Ortennasalor B. Mander B. Tampa, H., Mander H. M. Ortennasalor B. Mander B. Tampa, H., Mander H. M. Ortennasalor B. Mander B. Tampa, H., Mander H. M. Ortennasalor B. Mander B. Man		e e yA_site

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Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Submitssion (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tels1-438-2-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                        PRI 01-AUG-2002
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YNNELPWYRKGTVLIWQKVDEVWTKEIKLPTEMEGKKMAVTRTRTKPVPLHCDIIGDA
  644 GCTGCAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTACTGGTGTTAGTCCCAGATTGTTG 586
                                                                                                                                                                                                                                                                                                                                                                                                                       Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H., Wagatsuma, M., Hosoixi, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamarsu, Y., Nagahari, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T. NEDO human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                       Craniata, Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                          oligo capping; fis (full insert sequence)
Homo sapiens ovary, tumor tissue cDNA to mRNA, clone_lib:OVARC1
clone:OVARC1001188.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 AGGAACCATGTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGAGTACACCA
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                                                                                                                                                     AK023355 1780 bp mRNA linear
Homo sapiens cDNA FLJ13293 fis, clone OVARC1001188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="ovary, tumor tissue"
/clone Tib="OVARC1"
/note="cloning vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 504; DB 9; I
Pred. No. 1.4e-133;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="OVARC1001188"
                                                                                                                                                                                                                                                                                                                                                       Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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al Similarity 93.0%;
555; Conservative (
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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Best Local Similarity
Matches 555; Conserv
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AK023355/c
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JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
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Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Mnistry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mmgackvkvhdslatisitlervlelgatwakskfeyvrdfead
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ILFSEPNOINYNNEPBPMTKGTVLIWQKVDEVMTKEIKLPTEMEGKKWAVTRTFTKPVP
LHCDIIGDAFWKEHPEILDEDS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 CCCCCATCCATCCTTCCTTCCCTGTTCCCCTCCCAAC - TTGAGTTGTGTCATTCGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            944 AGGCTTGCATGGTTAAGCACACAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCT
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Pred. No. 1e-154;
0; Mismatches 5; Indels 2;
                                                                                                                                                                                                                                                                                                                                                       /tissue type="whole embryo, mainly head"/clone_lib="HEMBA1"
                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="embryo, 10 weeks"
/note="cloning vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      4. .900
/note="unnamed protein product"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /proteIn_id="BAB13870.1"
/db_xref="G1:10432894"
                                                                                                                                                                                                                                                          1. .2263
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEMBA1003893"
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Location/Qualif 1.15344 1.15344 Momo Corganism="Homo LanconSome="5" Chromosome="5" Clone="5" Clone="5" Clone="5" Clone="5" Clone="5" Clone="5" Clo	Best Local Similarity 98.9%; Pred. No. 4.1e-117; Matches 450; Conservative 0; Mismatches 5; Indels 0; Gaps 2 TGGAATGTTCTTGCTTTAAAAATAGTACTGCGATTAAAAAAAA	108014 122 108074	Oy 182 GTGTCCTGGTTGGTACAGGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGAG 241 Db 108134 GTGTCCTGGGTGGTAGTGCTACAGCCACCTAAGGAGGGGGGGG	Qy 302 AATCTCTGGATGTTCCTTCCAGAAAGCATCCCGGATGATATCGCAGTGCAAGGGCACTGG 361 	Qy 362 CTTTGTCCTGGTCCGGGTCACTGTTTTTCCTTCGTTGGCAGCTTAAT 421	RESULT 10 HUMZD93F03/C LOCUS HUMZD93F03/C DEFINITION Homo sapiens full length insert cDNA clone ZD93F03. ACCESSION AF086486 VERSION AF086486.1 GI:3483831 KEYMORDS FIL_CDNA SADIENS SOURCE HOMO SADIENS.	NISM Homo sapi Bukaryota, Mammalia, NCE Moessner, ORS Woessner, Marth,G., Geisel,S., Gibbons,M.	Milson, R. and Waterston, R. TITLE Full Clone Sequencing of the Longest Available Member from Each Unique Cluster JOURNAL Unpublished REFERENCE 2 (bases I to 416) AUTHORS Waterston, R. TITLE Direct Submission JOURNAL Submitted (24-AUG-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA COMMENT SUBMITTED BY:
CCCCCATCCATCCTTCCTTCCTGTTCCCCTCCCAACTTGAGTTGTGTCATTGGCACCA GTGTCCTGGGTGGGATGCTACAGCCACCTAAGGCAAGGAGGCCCTGGGAGGTGGGAG	302 ARICTCTGGATGTTCCAGAAGGATCCCGATGATGGATGGATGG	422 TTCTTTGTCATCACCTCACCTTCTGCCATATCAACACAGGTCCCTTTCCTATACAT 481	y 542 TGNAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTACTGGTGTTAGTCCAGATTGTTG 598	CCZ640/ OCUS AC026407 155344 bp DNA linear PRI 30-AUG-2001 OCUS AC026407 clone 5 clone CTC-370J7, complete sequence. CCESSION AC026407 GI:15375158	EYWORDS HTG. Homo sapiens. ORGANISM Homo sapiens. ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Cranïata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. BFERENCE 1 (bases 1 to 155344) AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center. TITLE Direct Submission		AL RS	www.jgl.doe.gov Finishing Completed at Stanford Human Genome Center Finishing Completed at Stanford Human Genome Center www-shoc.stanford.edu Quality: Phrap Quality >=40 99.8% of Sequence; Estimated Total Number of Errors is 0.2. STS Content: WI-11894 G13180 WI-6759 G05738 SHGC-58349 G38490 SHGC-57583 G37344.

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241 GGGCTTGCATGGTTAAGCACACCAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AAGGAACCATGTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 ACCCCCATCCATCCCTTCCTTCCCTCCCCAACTTGAGTTGTGTCATTCGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ACCCCATCCATCCTTCCTTCCTGTTCCCCTCCCAACTTGAGTTGTGTCATTCGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 AGTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGA
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                                                                                                                                                                                                                                                                                                                                         seconds
seconds
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Pred. No. 2.3e-95;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                    Initial incubation: 95 degrees C for 10 minutes
                                                                                                                            Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu
Primer A: CAACACCGCAAACAGGTGT
Primer B: GCTTAACCATGCAAGCCCTC
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75. .258
                                                                                             Contact: Richard M. Myers
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Annealing:
Polymerization:
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Thermal Cycler:
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Best Local Similarity 99.5%;
Matches 372; Conservative
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PCR Profile:
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SHGC-58349 Human Homo sapiens STS genomic, sequence tagged site.
G38490
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                                                                                                                          NOTICE: This sequence represents the full insert of this CDNA. No attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived. We have tried to obtain double stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved.

Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db xref="taxon:9606"
/clone='ImAGE:357053"
/clone lib="Soares fetal heart_NbHH19W"
91 c 109 g 103 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.0%; Score 406.4; DB 9;
99.8%; Pred. No. 1.4e-105;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                           The location of this clone is unknown
                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
             Department of Genetics
Washington University
St. Louis NO 63108, USA
http://genome.wustl.edu/gsc
mailto:est@watson.wustl.edu
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us-09-914-191-1.rge

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Direct Submission

Listing Submission

List Submission

List Submission

Cambridgeshire, CB10 15A, UK. E-mail enquiries:

Cambridgeshire, CB10 15A, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

Con Feb 21, 2002 this sequence version replaced gi:1849138

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may note be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the

assembly was confirmed by restriction digest. The following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL645948 207877 bp DNA linear ROD 16-FEB-2002 Mouse DNA sequence from clone RP23-298M7 on chromosome 11, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 317 TTCTTTTGTCATCACTTCATCCACCTTCTGCCATATCAACACAGTCCCTTTCCTATACAT 376
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                                                                              62 AGGAACCATGTTCCAACACGCGAAACAAGGTGTTCTGCTTAAAACAGAGTAAGATACACCA 121
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 207877)
Phillimore, B.
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                      CTTTGTCCTGGTCCGGGTCACTGCCATCTTTTTCCTTCCATTTCTGTTGGCAGCTTAAT
  GTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGGCCCTGGGAGGTGGGAG
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ALG45948.10 GI:18855237
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GAATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTG 360
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 567)
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Pred. No. 6.5e-77;
0; Mismatches 6; Indels 111;
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Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="5"
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119 g
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Primer A: CAACACCGCAAACAAGGTGT
Primer B: TCCTTGCCTTAGGTGGCTGT
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Thermal Cycler:
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                                                                                                                 361 GCTTTGTCCTGGTC 374
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Unpublished (1997)
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Best Local Similarity 79.0
Matches 440; Conservative
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Profile:
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BASE COUNT 1
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AUTHORS
TITLE
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COMMENT
                                                                                                                                                                        RESULT 12
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KEYWORDS
SOURCE
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AC073495.12 GI:10801940
HTG; HTGS PHASE1; HTGS_DRAFT,
Mus musculus.
Mus musculus
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    VERSION
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                                                                        http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-298M7 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VBCTOR: pBACe3.6

This sequence is the entire insert of clone RP23-298M7 The true left end of clone RP23-299H5 is at 164150 in this sequence. The true right end of clone RP23-302J15 is at 69639 in this sequence.
abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; WP:, WORWPEP; Information on the WORWPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318930 bp DNA linear HTG 15-OCT-2000 Mus musculus chromosome 11 clone RP23-345K4, WORKING DRAFT AC073495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="Sequence from uni-directional primer reads and dGTP in dve Perminator reads only."
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/note="Sequence from overlapping clone RP23-29H5
(AL663031). Assembly confirmed by restriction digest."
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/note="Sequence from overlapping clone RP23-29H5
(AL663031). Assembly confirmed by restriction digest."
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/note="Sequence.from uni-directional dGTP big dye
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                                                                                                                                                                                                                                                                1. .207877
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="11"
/clone="RP23-298M7"
                                                                                                                                                                                                                                                                                                                                                                                                                                      terminator reads only."
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72.7%;
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Matches 271; Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 318930)

"RS Metaker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C., Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T., Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J., Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z., Cox, C., Perraguto, D., Forcum-Tansey, J., Glil, R., Fornandez, C., Ferraguto, D., Haller, G., Hernandez, J., Hogues, M., Hosak, H., Hou, X., Huber, J., Jackson, L., Vally, J., Kelly, S., Kovar, C., Liu, J., Liu, W., Loulseged, H., Loado, R., Martin, R., Massey, E., McLeod, M. P., Mei, G., Moore, S., Morgan, M., Martin, R., Perez, L., Reiter, D., Say, J., Shen, H., Voguh, M., Parish, B., Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, L., Watlington, S., Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A., Watler, G., Zhou, X., Bouck, J., Hodgson, A., Watler, S., Sodergren, E., Weinstock, G., Direct Suhmissision
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Chemistry: Dye-brinder Big Dye: 29% of reads
Assembly program: Phrap; version 0.99329
Consensus quality: 28627/ bases at least Q40
Consensus quality: 309271 bases at least Q20
Consensus quality: 309271 bases at least Q20
Estimated insert size: 298164; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; agarose-fp estimation
Quality coverage: 5.1x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (19-JUN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Oct 15, 2000 this sequence version replaced gi:10800205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (see http://www.ngsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently consists of 64 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 61 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N. but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length
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------ Genome Center
Center: Baylor College of Medicine
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                                                                                       Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                            Center clone name: CH230-92F20
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), *** SEQUENCING IN PROGRESS
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                          384 GCCATCTTTTTCCTTCCATTTCTGTTGGCAGCTTAATTTCTTTTTTTCATCATCATCC
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504 ATGITGAATTCAGAAACAAATCTCATTCTTGTCTGCTGNAAGAGTTCCCTG 556 Search completed: July 12, 2003, 14:05:19 Job time : 1250 secs

444 ACCITCTGCCATATCAACACAGTCCCTTTCCTATACATCGGCAGCTCATTATATAGTTG 503

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Human cDNA clone (Human prostate exp Human prostate exp

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Identifying genes used for identifying drugs for the prevention and/or therapy of diabetic nephropathy involves culturing mesangial cells in
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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                                                                                                  glucose 1) cDNA partial sequence. THG-1 was identified using a novel method for identifying genes that have a role in the presentation of diabetic nephropathy (DN). This method involves culturing measangial cells in a medium in the presence of a concentration of glucose sufficient to induce differential expression of a gene susceptible to such differential expression, and identifying the gene so induced, especially by suppression subtractive hybridisation. Further portions of IHG-1 cDNA are given in AAA50409 and AAA50410. Genes identified by this method, including IHG-1, can be used as a diagnostic marker for the progression and presentation of DN, as an index of disease activity and the rate of progression of DN, and as a basis for identifying drugs for use in the prevention and/or therapy of DN (claimed).
                                                                   that of a human IHG-1 (increased in high
presence of glucose which induces differential expression of
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                                                  Claim 8; Page 7-8; 86pp; English.
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AAIS7967/c ID AAIS7967 standard, cDNA, 1231 XX AAIS7967, Xy,

RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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                                                                gene therapy; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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Zhang
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 597; DB 22;
Pred. No. 6.3e-174;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen R, Ma Y, (Xu C, Xue AJ, Y, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 170; 10078pp; English.
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                                polynucleotide SEQ ID NO 170.
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Wang Z, Wehrman T, X
Zhou P, Goodrich R,
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25-ARR-2000; 2000US-0552117.
09-UUL-2000; 2000US-059042.
19-UUL-2000; 2000US-0623150.
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19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
                                                                                                                                                                                                                                                                26-DEC-2000; 2000WO-US34263
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Best Local Similarity 99.8'
Matches 597; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
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Wang J,
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prostate expression marker cDNA 28674.
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Best Local Similarity 99.7%;
Matches 595; Conservative
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                                                                                                                                                                  TCGGCAGCTCATTATATAGTTGATGTTGAATTCAGAAAACAAAATCTCATTCTTGTCTG 540
                                                                                                                                                                                                                                   cytostatic; carcinogen; pharmacodyanamic marker; gene; 88.
                                                                                                                                                                                                                                                             CTGNAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTACTGGTGTTAGTCCAGATTGTTG 598
                                                                                                                                                                                                                                                                                624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
            ACCCCCATCCATCCCTTCCTTCCCTGTTCCCCTCCCAACTTGAGTTGTGTTTTGCCCCCC
ACCCCCATCCATCCTTCCTTCCTGTTCCCTCCCAACTTGAGTTGTGTCATTCGCACC
                                     AGTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGA
                                                GGGCTTGCATGGTTAAGCACACAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTA
                                                                                         GGGCTTGCATGGTTAAGCACACCAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTA
                                                                                                            GAATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTG
                                                                                                                              GAATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTG
                                                                                                                                                TTTCTTTTGTCATCACTTCCACCTTCTGCCATATCAACACAGTCCCTTTCCTATACA
                                                                                                                                                                                                                                                                        CTGCAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTACTGGTGTTAGTCCAGATTGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 4042; 11750pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monahan JE;
                                                                                                                                                                                                                                                                                                                    ABV22854/c
ID ABV22854 standard; cDNA; 1512
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; 2000US-189862P.
; 2000US-207454P.
; 2000US-211314P.
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                                                                                                                                                                                                                                                                                                                                                                                                       Human; prostate cancer;
pharmacogenomic marker;
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121
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1246 GGCTTGCATGGTTAAGCACACCAGAACTGAAGGGCAAAAGGGTCAGCTGTCTTCATCTAG 1187
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                                                                                                         (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              947
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(I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
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Pred. No. 4.4e-173;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1512 BP; 407 A; 327 C; 401 G; 356 T; 21 other;
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1186 AATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTGG 1127
                                                                                                                                                                                                          1066 TTCTTTTGTCATCACTTCATCCACCTTCTGCCATATCAACACAGTCCCTTTCCTATACAT 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence and an oligonuclectide comprising a sequence complementary to a polynuclectide which comprises a 3'-end sequence, where the oligonuclectide comprises at least 15 nuclectides and the combination of the 5'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                      598
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                                                                                                                 1126 CTTGTCCTGGTCCGGGTCACTGCCATCTTTTTCCTTCCATTTCTGTTGGCAGCTTAAT
                                                                                                                                                                                                                                                                                               1006 CGGCGGCTCATTATTATAGTTGATGTTGAATTCAGAAAACAAAATCTCATTCTTGTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; primer; detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                 TTCTTTTGTCATCATCCATCCATCTGCCATATCAACACAGTCCCTTTCCTATACAT
                                                                                                                                                                                                                                                     482 CGGCAGCTCATTATTATAGTTGATGTTGAATTCAGAAAACAAAATCTCATTCTTGTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs
                 542 TGNAAGAGTTCCCTGTAATCTCCCTTGGCCTTGTACTGGTGTTAGTCCAGATTGTTG
                                                                                                                                                                                                                                                                                                                                                            Yamamoto
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Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; SEQ ID 10648; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA sequence SEQ ID NO:10648
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11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                     422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
cytostatic; carcinogen; pharmacodyanamic marker;
gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGAACCATGTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 6017; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Monahan JE;
                                                                                                                                                                                                                                                                     2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
                                                                                                                                                                                                          20-FEB-2001; 2001WO-US05171.
                                                                                                                                                                                                                                                                                                                                                            2000US-255281P.
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nes 595; Conservative
                     Human; prostate cancer;
pharmacogenomic marker;
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                                                                                                                         WO200160860-A2
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16-MAR-2000;
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in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13639 to AAH13639 to AAH13639 to AAH36393 represent human cDNA sequences; AAB92446 to AAH3632 represent bunan amino acid sequences; and AAH13632 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
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                                                                                                                                                                                                                                      Score 591.2; DB 22; Length 2159;
Pred. No. 5.1e-172;
0; Mismatches 4; Indels 0;
                                                                                                                                                                                                  Sequence 2159 BP; 607 A; 463 C; 522 G; 567 T; 0 other;
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.3%;
Matches 593; Conservative
                                                                                                                                                             the present invention.
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1064 CCCCCATCCATCCCTTCCTTCCTGTTCCCTCCCAACTTTTTGTTGTGTCATTCACAC
Query Match 96.6%; Score 577.6; DB 22; Length 2263; Best Local Similarity 98.8%; Pred. No. 8.4e-168; Matches 592; Conservative 0; Mismatches 5; Indels 2;
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                                                                                                                                                                                                                                              SEQ ID NO:13474.
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                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                               26-JUN-2001
                                                                                                                                                                                                                                              Human cDNA
                                                                                                                                                                                 AAH15315;
                                                                                                                       RESULT 6
AAH15315/c
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Sequence 2263 BP; 624 A; 486 C; 580 G; 573 T; 0 other;

Gaps

AGGAACCATGTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGAGTAGAAGATACACCA

CCCCCATCCATCCCTTCCCTGTTCCCCTCCCAAC--TTGAGTTGTGTCATTCGCAC

AGGAACCATGTTCCAACACGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACCA

239 945

CAGTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGG

cagneric regeneración a consecuencia de consecu AGGGCTTGCATGGTTAAGCACACAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCT 944 AGGGCTTGCATGCTTAAGCACACAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCT

240

EP1074617-A2

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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comptises: (a) an oligo-dT primer and an oligounclectide complementary to the complementary strand of a polynuclectide which comprises one of the 5602 nuclectide sequences defined in the specification, where the oligonuclectide comprises at least 15 nuclectides; or (b) a combination of an oligonuclectide comprising a sequence complementary to the complementary strand of a polynuclectide which comprises a 3'-end sequence complementary to the complementary strand of a polynuclectide which comprises a 3'-end sequence complementary to a polynuclectide which comprises a 3'-end sequence complementary to a polynuclectide comprises at least 15 nuclectides and the comprise oligonuclectide some sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers are useful for synthesising polynuclectides, particularly full-length cDNAs. The primers are also useful for the proteins encoded by the full-length without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH13633 to AAH13633 to AAH13632 to AAH13632 to AAH13632 to AAH13633 to AAH13632 to AAH13632 to AAH13633 to AAH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                       Yamamoto
                                                                                                                                                                                                                                                                                                                                                       Saito K,
Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; SEQ ID 13474; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                       Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                       hikawa T,
Wakamatsu
                                                                                                                                                                                                                                                                                                                                                 sogai T, Nishikawa
Sugiyama T, Wakama
                                                                                                                                        27-AUG-1999; 990P-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
                                                                                                                                                                                                                                   09-JUN-2000; 2000JP-0241899
                                                         2000EP-0116126
                                                                                                                                                                                                                                                                                             (HELI-) HELIX RES INST.
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                                                                                                                                                                                                                                                                                                                                                    Isogai T,
                                                         28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                    Ota T, Is
Ishii S,
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for

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N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-2000; 2000EP-0116126
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99JP-0300253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                            Best Local Similarity 99.8
Matches 541; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TG 543
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27-AUG-1999;
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                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P cypression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing in a patient's genome that affect the activity of P by expressing in active proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB37789 represent sequences used in the exemplification of the present invention.
                                                                                                        479
                                                       419
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                                                                                                                                                                          AGAATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACT 359
                             825
                                                                             764 ATTICTTTTGTCATCATCATCCACCTTCTGCCATATCAACACAGTCCCTTTCCTATAC 705
                                                                                                                                                                                                            598
                                                                                                                                                                                                                         644 GCTGCAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTACTGGTGTTAGTCCAGATTGTTG 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                  ATTICITITGECATCACTICATCCACCTTCTGCCATATCAACACAGTCCCTTTCCTATAC
                                                                                                                                                          ATCGGCAGCTCATTATATAGTTGATGTTGAATTCAGAAAACAAAATCTCATTCTTGTCT
                                                                                                                                                                                                          540 GCTGNAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTACTGGTGTTAGTCCAGATTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                      colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                          Human colon cancer antigen encoding cDNA SEQ ID NO:958.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 2854; 9803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birse CE,
                                                                                                                                                                                                                                                                    RESULT 7
AAH33902/c
ID AAH33902 standard; cDNA; 557 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0157137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-SEP-2000; 2000WO-US26524
                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                    colorectal carcinoma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-235357/24.
P-PSDB; AAG74471.
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03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243
                                                                                                                                                                                                                                                AGGAACCATGTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATCTCTGGGATGTTCCTTCCAGAAAGCATCCCGGATGATATCGCAGTGCAAGGGCACTGG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTTGTCCTGGTCCGGGTCACTGCCATTTTTTTCCTTCCATTTCTGTTGGCAGCTTAAT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grerccrederecraedearecraedeceaecraagecaageceregeageregaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITCTITIGECATCACTTCCACCTTCTGCCATATCAACACAGTCCCTTTCCTATACAT 481
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                                                                                                                                                                              TGGAATAGTTCTKGCTTTATAAAAATAGTACTGCGATTAAAAAAAAGCACTTCTGCCAA
                                                                                                                                                                                                                                                                               AGGAACCATGTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACCA
                                                                                                                                                                                                                                                                                                                                                                               CCCCCATCCATCCATCCTTCCTTCCTTCCCTCCCCACTTGAGTTGTGTCATTCGCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 GGCTTGCATGGTTAAGCACACAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCTTTTGTCATCACTTCATCCACCTTCTGCCATATCAACACAGTCCCTTTCCTATACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGCAGCTCATTATTATAGTTGATGTTGAATTCAGAAAACAAAATCTCGTTGTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCTTGCATGGTTAAGCACACACAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; primer; detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGGAGGTGGGAG
                                                                                                   Gaps
                                                                                                .
0
                                              DB 22; Length 557;
                                                                                                0; Indels
Sequence 557 BP; 156. A; 111 C; 150 G; 139 T; 1 other;
                                            Score 541.6; DB 22
Pred. No. 5.6e-157;
                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA sequence SEQ ID NO:15323
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                                            90.6%;
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425 TTCTTTTGTCATCACTTCATCCACCTTCTGCCATATCAACACAGTCCCTTTCCTATACAT 366

422

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482

542 IGNAAGAGITCCCTGTAATCTCCCTTGGGCTTGTACTGGTGTTAGTCCAGATTGTTG 598 TGCAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTACTGGTGTTAGTCCCAGATGTTG 249

365 CGCCAGCTCATTATTATAGTTGATGTTGAATTCAGAAAACAAAATCTCATTCTTGTCTCC CGGCAGCTCATTATTATAGTTGATGTTGAATTCAGAAAACAAAATCTCATTCTTGTCTGC

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sequence and an oligonucleotide computation are determined propriated to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises a 1'-end sequence, where the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 represent human amino acid sequences; AAB95446 to AAH3632 represent tuman amino acid sequences; and AAH13629 to AAH13632 represent coligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                   full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                         Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                             Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes primer sets for synthesising 5602
                                                                                                                                          Saito K, Ye
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1780 BP; 513 A; 368 C; 435 G; 464 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                Claim 8; SEQ ID 15323; 2537pp + CD ROM; English.
                                                                                                                                          Hayashi K, S
A, Nagai K,
                                                                                                                                                                   Wakamatsu
                                                                                                                                          Nishikawa
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the present invention.
                                                                                              (HELI-) HELIX RES INST.
                                                                                                                                                                Ishii S, Sugiyama T,
                                                                                                                                                                                                             WPI; 2001-318749/34.
                                                                                                                                          Isogai T,
                                                                                                                                          Ota '
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Human, digestive system antigen, gene therapy, cancer, appendicitis, ulcerative colitis, infection, Hirschsprung's disease, chronic colitis, digestive system disorder, Meckel's diverticulum, ds.

Human digestive system antigen genomic sequence SEQ ID NO: 4401.

(first entry)

05-NOV-2001 AAK90825;

AAK90825 standard; DNA; 15865 BP

RESULT 9 AAK90825/c

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24-FEB-2000; 2000US-0184664.
02-MAR-2000; 2000US-0186350.
16-MAR-2000; 2000US-0189874.
17-MAR-2000; 2000US-0190076.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-AUG-2000; 2000US-0228924
                                                                                                                                  WO200155314-A2.
                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                       07-JUN-2000;
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14-AUG-2000;
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222
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                                                                                                                                                                                                                                                                                                                                                         AGGAACCATGTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACA 121
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                                                                                                                                                                                                                                                                                                                          CCCCCATCCATCCCTTCCTTCCTGTTCCCCTCCCAACTTGAGTTGTGTCATTGCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCTTGCATGGTTAAGCACACCAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 605 GCCTTGCATGCTTAAGCACACAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTAG
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                                                                                                                                                                                                                                                                                                              744 AGGAACCATGTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGGTGGGAGGTGGGAG
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                       41;
                                                                                                                                                                                                                                                                Score 504; DB 22; Length 1780;
Pred. No. 4.1e-145;
0; Mismatches 1; Indels 41;
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Best Local Similarity 93.0%;
Matches 555; Conservative 0
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PR 01-SEP-2000; 2000US-022943.

PR 01-SEP-2000; 2000US-022943.

PR 01-SEP-2000; 2000US-022943.

PR 05-SEP-2000; 2000US-022943.

PR 05-SEP-2000; 2000US-022943.

PR 06-SEP-2000; 2000US-022943.

PR 06-SEP-2000; 2000US-023943.

PR 06-SEP-2000; 2000US-0231443.

PR 06-SEP-2000; 2000US-0231443.

PR 06-SEP-2000; 2000US-0231443.

PR 06-SEP-2000; 2000US-0231443.

PR 14-SEP-2000; 2000US-0231443.

PR 14-SEP-2000; 2000US-0231306.

PR 14-SEP-2000; 2000US-023399.

PR 25-SEP-2000; 2000US-023499.

PR 25-SEP-2000; 2000US-023499.

PR 25-SEP-2000; 2000US-023499.

PR 25-SEP-2000; 2000US-023499.

PR 25-SEP-2000; 2000US-0234647.

PR 25-SEP-2000; 2000US-0234647.

PR 25-SEP-2000; 2000US-0234647.

PR 25-SEP-2000; 2000US-0234652.

PR 25-SEP-2000; 2000US-0234652.

PR 25-SEP-2000; 2000US-0234652.

PR 25-SEP-2000; 2000US-024652.

PR 25-SEP-2000; 20
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PR 17-NOV-2000; 2000UGS-0249212.
PR 17-NOV-2000; 2000UGS-0249214.
PR 17-NOV-2000; 2000UGS-0249214.
PR 17-NOV-2000; 2000UGS-0249215.
PR 17-NOV-2000; 2000UGS-0249216.
PR 17-NOV-2000; 2000UGS-0249218.
PR 17-NOV-2000; 2000UGS-0249218.
PR 17-NOV-2000; 2000UGS-0249218.
PR 17-NOV-2000; 2000UGS-0249218.
PR 17-NOV-2000; 2000UGS-0249265.
PR 17-NOV-2000; 2000UGS-0249299.
PR 17-NOV-2000; 2000UGS-0249299.
PR 17-NOV-2000; 2000UGS-0249299.
PR 17-NOV-2000; 2000UGS-0249299.
PR 17-NOV-2000; 2000UGS-025939.
PR 17-NOV-2000; 2000UGS-025968.
PR 17-NOV-2000; 2000UGS-025999.
PR 17-NOV-2000; 2000UGS-025968.
PR 17-NOV-2000; 2000UGS-025999.
PR 17-NOV-2000UGS-025999.
PR 17-
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14538 62 AGGAACCATGTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACCA 121 14597 CCCCCATCCATCCATCCTTCCCTGTTCCCCTCCCAACTTGAGTTGTGTCATTCGCACCA CCCCCATCCATCCCTTCCCTGTTCCCCTCCCCAACTTGAGTTGTGTCATTCGCACCA GTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGAG 14537 GIGICCIGGGIGGIAGGGAIGCIACAGCCACCIAAGGCAAGGAGCCCIGGGAGGIGGGAG GGCTTGCATGGTTAAGCACACACAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTAG The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention. · 0 Query Match

74.7%; Score 447; DB 22; Length 15865;
Best Local Similarity 98.9%; Pred. No. 5.1e-127;
Matches 450; Conservative 0; Mismatches 5; Indels 0; Sequence 15865 BP; 4775 A; 3204 C; 3309 G; 4577 T; 0 other; 122 182 242 ~

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                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes primer sets for synthesising 5602

(ull-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligonuclectide complementary
to the complementary strand of a polynuclectide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
oligonuclectide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 3'-end sequence.
C gequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a sequence is selected from those defined in
the 5'-end sequence/3'-end sequence is selected from those defined in
the 5'-end sequence/3'-end sequence is selected from those defined in
the specification. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
characterion and/or diagnosis of the abnormality of the proteins encoded by
the full-length without any specialised methods. AAM133166 to AAM13528 and
AAM13633 to AAM18742 represent human cDNA sequences; AAB92446 to
                                                                      14417 AATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTGG 14358
                                                         421
                                                                                                                                                                                                                                                                                     Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss
                                                         CTTTGICCTGGICCGGGICACTGCCATCTTTTTCCTTCCATTTCTGTTGCCAGCTTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamamoto J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saito K,
, Otsuki 1
                                                                                                                    14297 TTCTTTTGTCATCATCATCCACCTACAGGTAAA 14263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID 3986; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashi K, S
A, Nagai K,
                                                                                                      TTCTTTTGTCATCACTTCATCCACCTTCTGCCATA
                                                                                                                                                                                                                                                               SEQ ID NO:3986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isogai T, Nishikawa T,
                                                                                                                                                                                       AAH07151 standard; cDNA; 618 BP
                                                                                                                                                                                                                                                                                                                                                                                                                      99JP-0300253.
2000JP-0118776.
2000JP-0183767.
                                                                                                                                                                                                                                                            Human cDNA clone (5'-primer)
                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000JP-0241899
                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JUN-2000;
                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                      EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                            29-JUL-1999;
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                                                       362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259
                     represent oligonucleotides, all of which are used in the exemplification
AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
                                                                                                                                                                                                                                                                  CATTCTTGTCTGCTGCAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTACTGGTGTTAGTC
                                                                                                                                                                                                                                   TGGGAGGTGGGAGGGCTTGCATGGTTAAGCACACCAGAAACTGAAAAGGGTCAGC
                                                                                                                                                                                                                                                                                                                               TGTCTTCATCTAGAATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGGATGATATCGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                       TTGGCAGCTTAATTTCTTTTGTCATCACTTCCACCTTCTGCCATATCAACACAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGGCAGCTTAATTTCTTTTGTCATCACTTCATCCACCTTCTGCCATATCAACACAGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTTCCTATACATCGCCAGCTCATTATTATAGTTGATGTTGAATTCAGAAAACAAATCT
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                                                                                                                                                                                       Gaps
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                                                                                                                                                                                    ö
                                                                                                                                        Length 618;
                                                                                                                                                                                    5; Indels
                                                                                          Sequence 618 BP; 186 A; 135 C; 145 G; 149 T; 3 other;
                                                                                                                                      22;
                                                                                                                                 Score 364.4; DB 22
Pred. No. 3.4e-102;
                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; nootropic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human polynucleotide SEQ ID NO 3742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAIS97S3/c
ID AAIS97S3 standard; cDNA; 1103 BP.
                                                                                                                                                         98.68;
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2000US-0598042
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14-SEP-2000; 2000US-0662191
19-OCT-2000; 2000US-0693036
29-NOV-2000; 2000US-0727344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0488725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0620312
                                              the present invention.
                                                                                                                                                                                  Matches 365; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGATTGTTG 598
                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200153312-A1
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09-JUL-2000;
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expressed in cancer tissues. ABB78993 to ABB78004 represent proteins encoded by the AB806177 to AB878993 to ABB780004 represent proteins canced by the AB806177 to AB878993 to ABB780004 represent proteins canced by the AB806177 to AB8760787 incleic acid sequences. (1) can be encoded by (1) is useful for detecting cancer in a patient sample, and nucleic acid which hybridises to (1) in a cell. A probe/primer derived from (1) can be used for determining the presence of a nucleic acid which hybridises to (1) in a cell. A probe/primer derived from (1) can be used for determining the phenotype of cells in a sample of cells from a patient. (1) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence of state of other type of cancer, in antisense therapy, to generate macroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profiling, forensics, genetic analysis, mapping and diagnostic applications. (1) can be used to raise antibodies, and to screen for peptide analogues and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 CCTCCCAACTTGAGTTGTGTCATTCGCACCAGTGTCCTGGGTGGTAGGGATGCTACAGCC 210
                    66. GCTGCAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTACTGGTGTTAGTCCAGATTGTTG 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 ACTGCGATTAAAAAAAAAGCACTTCTGCCAAAGGAACCATGTTCCAACACGCAAACAAG 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ACTGCGATTAAAAAAAAGCACTTCTGCCAAAGGAACCATGTTCCAACACGCGAAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid that is differentially expressed in cancer tissues useful for determining the presence of colon cancer in a cell or tissue type, and in antisense therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dwivedi P, Molino GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
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                                                                                                                                                                                                                                                                                         Human colon cancer related nucleotide sequence SEQ ID NO:2304
                                                                                                                                                                                                                                                                                                                                Human; colon cancer; cancer; tissue profiling; forensic; r
genetic analysis; diagnostic; antisense therapy; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.0%; Score 322.8; DB 24; Length ilarity 97.5%; Pred. No. 1.9e-89; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 361 BP; 91 A; 102 C; 81 G; 82 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Catino TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carroll E,
                                                                                                                                                        ABQ58609 standard; cDNA; 361 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-OCT-2001; 2001WO-US30732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-OCT-2000; 2000US-237271P.
                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 1; 796pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burgess C, Astle JH,
Thiaglingam A, Lewis
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Best Local Similarity
Matches 346; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-426115/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200229086-A2.
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                             02-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-APR-2002.
  540
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                                                                                                                                                                                                   ABQ58609;
                                                                                                            RESULT 12
                                                                                                                                   ABQ58609
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                                                                                                                                                                                                                                                                                                           The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                       system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
                                              ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1038 AGGAACCATGTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGAGAGTAAGATACACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 AGGAACCATGTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGGAGTAAGATACACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCCCATCCATCCTTCCTTCCCTGTTCCCCT-CCCAACTTGAGTTGTGTCATTCGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AGTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCC-TGGGAGGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTGTCCTGGGTGGTAGGATGCTACAGCCACCTAAGGCAAGGAGCCCTTGGGAGGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 AGGGCTTGCATGGTTAAGCACACAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    420 ATTTCTTTTGTCATCACTTCATCCACCTTCTGCCATATCAACACAGTCCCTTTCCTATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCGGCAGCTCATTATTATAGTTGATGTTGAATTTCAGAAAACAAAATCTCATTCTTGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 344.4; DB 22; Length 1103;
Pred. No. 6.9e-96;
0; Mismatches 2; Indels 111; Gaps
                                              Wang
                                                                                                                                                                                                   Novel nucleic acids and polypeptides, useful for treating disorders
                                           Ren F, W
Zhang J;
                                           Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1103 BP; 303 A; 242 C; 290 G; 268 T; 0 other;
                                         Liu C, Asundi V, Chen R, Ma Y,
Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 3742; 10078pp; English.
                                                                                                                                                                                                                          such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.6%;
81.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 486; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                 WPI; 2001-442253/47.
(HYSE-) HYSEQ INC
                                                                                                                                                        P-PSDB; AAM40597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   848 -----
                                         Tang YT,
Wang J, V
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122
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Length 390;

23; .7e-70; 38; 430

ABV13617/c RESULT 13

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88.

Yamamoto J;

Saito K, Otsuki

Claim 1; SEQ ID 561; 2537pp + CD ROM; English.

is also useful as a pharmacodyanamic or pharmacogenomic marker.

Sequence 390 BP; 126 A; 74 C; 104 G; 86 T; 0 other;

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GATGCTTCAACCCCCTAAGGCCAGGAGCCCTTGGAAGGTTGGAAGGCTTGCATGGTTTA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATTATTATATGTTGATGTTGAATTCAGAAAACAAAATCTCATTCTTGTCTGCTGNAAGAG 549
                                                                                                                                                                                     GCACA-CCAGAACTGAAGCGCAAAAGGGTCAGCTG----TCTTCATCTAGAATCTCTGGA 311
                                                                                                                                                                                                                                                                                                   GTICCTICCAAAAAGCATICCCCATGATATCGCAGTGCAAGGGCCCTGGCTTTGTCCTG 211
                                                                                                                                                                                                                                                                                                                                                                                 Greedercaerecearerrrrreerreearreeredeagerraarrrerrer 151
                                                                                                                                                                                                                             GCCCCCCCCAGAACTTAAGCGCCAAAAGGGTCAACTGTTTTTTCATCTTAAAATTTTCTGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATTATTATAGTTGGTGGAATTCAGAAAACAAAATCTCATTGTTGCTGCAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATCACTTCATCCACCTTCTGCCATATCAACACAGTCCCTTTCCTATACATCGCGGGGCT
                                                                                                                                                                                                                                                                  TGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTGGCTTTGTCCTG
                                                                                                                                                                                                                                                                                                                                              GTCCGGGTCACTGCCATCTTTTTTCCTTCCATTTCTGTTGGCAGCTTAA-TTTCTTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                           431 CATCACTTCAT-CCACCTTCTGCCATATCAACACAGTCCCTTTCCTATACATCGGCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; primer; detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length DNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                     GATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGA--GGTGGGAGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nikawa T, Hayashi K, Sa
Wakamatsu A, Nagai K,
                                                             0; Mismatches
                      Score 259.8;
Pred. No. 5.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cDNA clone (5'-primer) SEQ ID NO:561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TICCCTGTAATCTCCCTTGGGCTTGTAC 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCCCTGTAATCTCCCTTGGGCTTGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH03726 standard; cDNA; 856
                          43.4%;
llarity 87.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-318749/34.
                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP1074617-A2
                          Query Match
Best Local Simi
Matches 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ota T, Iso
Ishii S,
                                                                                                                                            390
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                                                             270
                                                                                                     240
                                                                                                                                                                   AAGCGCAAAAGGGTCAGC-TGTCTTCATCTAGAATCTCTGGATGTTCCTTCCAGAAAGCA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogent protential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
CTCCCCAACTTGAGTTGTGTCATTCGCACCAGTGTCCTGGGTGGTGGTAGGATGCTACAGCC
                                                                                    ACCTAAGGCAAGGAGGCCCTGGGAGGTGGGGGTTGCTTAAGCAACACCACAGAACTG
                                                             ACCTAAGGCAAGGAGCCCTGGGAGGTGGGAGGGCTTGCATGGTTAAGCACACCAGAACTG
                                                                                                                                                                                                                        383
                                                                                                                                                                                                                      TCCCCGATGATATCGCAGTG-CAAGGGCACTGGCTTTGTCCTGGTCCGGGTCACT
                                                                                                                                                                                                                                                 TCCCCNATGATATCGCANTGCCAAGGACACTGNCTTTGGCCTGGTCCGGNTCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human prostate expression marker cDNA 13608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 2258; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monahan JE;
                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-183319P.
2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
                                                                                                                                                                                                                                                                                                                                                             ABV13617 standard; cDNA; 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-FEB-2001; 2001WO-US05171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-255281P
                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schlegel R, Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-2002
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                                                                                                 181
                                                                                                                                        271
                                                                                                                                                                               241
                                                           211
                                                                                                                                                                                                                      330
                                                                                                                                                                                                                                                            301
                                                                                                                                                                                                                                                                                                                                                                                                    ABV13617;
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence confilementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the comprises at least 15 nucleotides and the combination of the 5'-end sequence 3'-end sequence, where the oligonucleotide which comprises at least 15 nucleotides and the combination of the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the price of the full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the price of the full-length and seasily without any specialised methods. AAH313629 to AAH3632 and AAH3633 represent human amino, acid sequences; and AAH13629 to AAH33632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          329 ATCCCCGATGATATCGCAGTGCAAGGGCACTGGCTTTGTCCTGGTCCGGGTCACTGCCAT 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   617
                                                                                                                                                                                                                                                                                                                                                                                                           represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTGCCATATCAACACAGTCCCTTTCCTATACATCGGCGGCTCATTATATAGTTGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTTTTTCCTTCCATTTCTGTTGGCAGCTTAATTTC-TTTTGTCATCACTTCATCCACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTGCCATATCAACACAGTCCCTTTCCTATACATCGGCAGCTCATTATTATATGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rgaatrcagaaacanaarcrcatrcrrgrcrgcrgcaagagrrcccrgraarcrccrr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic; carcinogen; pharmacodyanamic gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22; Length 856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 856 BP; 248 A; 183 C; 222 G; 196 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 237.4; DB 22;
Pred. No. 7.1e-63;
----rhes 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGCTTGTACTGGTGTTAGTCCAGATTGTTG 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGCTTGTACTGGTGTTAGTCCAGATTGTTG 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human prostate expression marker cDNA 34722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.7%;
94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABV34731 standard; cDNA; 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-FEB-2000; 2000US-183319P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; prostate cancer;
pharmacogenomic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        568
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463
                                                                                                                                                                                                                                                                                                                                                                comprising
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(a) assessing whether a parient. (1) is useful for:
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(f) assessing the aggressiveness or indolence of prostate cancer in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                      Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTCCCTTTCCTATACATCGGCGCTCATTATTATATAGTTGATGTTGAATTCAGAAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGTTGGCAGCTTAA-TTTCTTTTGTCATCACTTCAT-CCACCTTCTGCCATATCAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cregrescascriaarrircrirrerrarcacricarccaccrircrescararcac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTCCCTTTCCTATACATCGGCAGCTCATTATTATAGTTGATGTTGAATTCAGAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 287 AGIGCAAGGGCCCIGGCTITGICCIGGICCGGGICACIGCCAICITITITCCTICCAITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATCTCATTCTTGTCTGCTGNAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTAC 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 AATCTCATTCTTGTCTGCTGCAGAGTTCCCTGTAATCTCCCTTGGGCTTGTAC 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 202.6; DB 23; Length
Pred. No. 2.3e-52;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346 AGIGCAAGGCACTGCCTTTGTCCTGGTCCGGGTCACTGCCATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 287 BP; 97 A; 55 C; 81 G; 54 T; 0 other;
                                                                                                                       (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                        Claim 1; Page 7273; 11750pp; English
                                                                                                                                                             Schlegel R, Endege WO, Monahan JE;
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                                     2000US-211314P.
2000US-219007P.
                                                                               2000US-255281P
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Best Local Similarity 97.0°
Matches 227; Conservative
                                                                                                                                                                                                  WPI; 2001-662795/76.
                                                                             13-DEC-2000;
                                     09-JUN-2000;
                    25-MAY-2000;
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DB 1; Length 7218;
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COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS: 62
STREET: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
            US-09-215-131-3

US-09-22-734-3

US-08-890-853-1

US-09-099-125A-1

US-09-125A-1

US-09-127-008-1

US-09-137-008-1

US-09-032-476-1

US-08-039-134-1

US-08-10-820-8

US-09-215-131-1

US-09-215-131-1
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-09-302-620B-82
                                                                                                                                                                                                                                                         US-08-961-083-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Foley & Lardner STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.1%; Score 48.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 899149
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (703)683-4109
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222668
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222268
339931
24145
74145
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EDNESS: single
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US-08-232-463-14
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IMMEDIATE SOURCE
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                                                                                                                                                                                                                                                                                                                                                                   US-08-232-463-14
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Query Match
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Sequence 101, App
                                                                                                                      (without alignments)
4168.016 Million cell updates/sec
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Sequence 1
Sequence 5
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Sequence
Sequence
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-453-274B-96
US-08-453-695A-96
US-08-268-161A-96
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PCT-US95-08071-96
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US-08-487-826B-1
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Maximum Match 100%
Listing first 45 summaries
                                                                          - nucleic search, using sw model
                                                                                                      July 12, 2003, 13:38:58
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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us-09-914-191-1.rni

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38854 CTTCTTCTTTTTTTTTTTTTTTTTTTTTGAGA 38819
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                                                                                                                                                                               6.6%; Score 39.2; DB 3;
53.2%; Pred. No. 0.048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UMBER: US/08/568,459A
07-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08568459A
Patent No. 5849306
  101:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peterson, David S.
                                                                                               TOPOLOGY: linear . MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Plasmodium vivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,6
                                      LENGTH: 43795 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sim, Kim L.
Chitnis, Chetan
Miller, Louis H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (619) 235-0176 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          83; Conservative
                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Mai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Newport Beach
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
FILING DATE: 07-DECCLASSIFICATION: 43:
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                                                                                                                                                                                                  Best Local Similarity
Matches 83; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Sim; Ki
APPLICANT: Chitnis
APPLICANT: Miller,
APPLICANT: PECETSO
APPLICANT: WELLEN
APPLICANT: Wellems
                                                           TYPE: nuclei
STRANDEDNESS:
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                                                                                      106 AGAGTAAGATACACCCCCCATCCCTTCCCTTCCCTGTTCCCCTCCCAACTTGAGT 165
                                                                                                                                           166 TGTGTCATTCGCACCAGTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGTTGGCAGCTTAATTTCTTTTGTCATCACTTCATCCACCTTCTGCCATATCAACACAG 465
                                                                                                                                                                                                                       226 CCCTGGGAGGTGGGAGGGCTTGCATGGTTAAGCACACCAGAACTGAAGCGCAAAAGGGTC
                                                                                                                                                                                                                                                                                                          286 AGCTGTCTTCATCTAGAAICTCTGGAIGTTCCTTCCAGAAAGCATCCCCGATGATATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
Best Local Similarity 4.1%; Pred. No. 1.5e-05;
Matches 16; Conservative 216; Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Hamilton, Brook, Smith & Reynolds, P.C.
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/742,185
FILING DATE: 30-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1417 YYYYYYYYYYYYYYYYYYYGTACCAAATTCTTCTA 1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         466 TCCCTTTCCTATACATCGGCAGCTCATTATA 499
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REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH194-07A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFRAX: (617) 861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/690,734
FILING DATE: 31-UUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/310,429
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 101, Application US/08742185
Patent No. 6020476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Reijo, Renee
APPLICANT: Reijo, Renee
APPLICANT: Saxena, Richa
APPLICANT: Hawkins Trevor
APPLICANT: Reeve, Mary Pat
TITLE OF INVENTION: DAZ: A GJ
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton. Brook
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDALL STREET: TWO ...
CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6020476
GENERAL INFORMATION:
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APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
WUMBER OF SEQUENCES: 37
                                                                                                                                                                                                   362 CTTTGTCCTGGTCCGGGTCACTGCCATCTTTTTCCTTCCATTTCTGTTGGCAGCTTAAT
                                                                                                                                                                                                                                                                        422 ITCTITIGICATCACTTCACCCTTCTGCCATATCAACACAGTCCCTTTCCTATACAT
Length 43795;
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APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
      TITITCCATCACATTITICTTTCAGTITITGCACTTCTGTGGGGCAATTCTGACACGTAAT 1557
                                                                                                                                                         1556 cécriccécarréregarcearérarararerecegricrararraceceaacarrra 1497
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                                                                                                  451 GCCATATCAACACAGTCCCTTTCCTATACATCGGCAGCTCATTATTATATGATGTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
CMCHUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
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Pred. No. 0.15
0; Mismatches
                                                                                                                                                                                                                                                                                      1496 ATTTACAAATCCATATAAAATTC 1474
                                                                                                                                                                                                                           511 ATTCAGAAACAAAATCTCATTC 533
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CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Knobbe Martens Olson
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09210288 Patent No. 6392026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium vivax
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Chitnis, Chetan
Miller, Louis H.
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Best Local Similarity 53.1%;
Matches 76; Conservative
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Fuller, Michael
REGISTRATION NUMBER: 36
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4084 base pairs
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STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Ma
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                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-210-288-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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APPLICANT:
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APPLICANT: Miler, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
APPLICANT: Petlems, Thomas E.
APPLICANT: APPLICA
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                                                                                                                               Gaps
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                                                              Length 4084;
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                                                                                                                            67; Indels
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Pred. No. 0.15;
0; Mismatches 67;
                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach STATE: California
                                                                                                                            0; Mismatches
                                                              Score 35.8;
Pred. No. 0.
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APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1496 ATTTACAAATCCATATAAAATTC 1474
                                                                                                                                                                                                                                                                                                                                                                                                                                             511 ATTCAGAAACAAAATCTCATTC 533
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OPERATING SYSTEM: CC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08487826B Patent No. 5993827
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NAME: Israelsen, Ned
REGISTRATION UNDRER: 29,655
REFERENCE/DOCKET NUMBER: NIH12
TELECOMMUNICATION INFORMATION:
TELEFRAX: (619) 235-8550
INFORMATION FOR SEQ ID NO: 1:
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                                                              6.0%;
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MEDIUM TYPE: Floppy disk
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LENGTH: 4084 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                Query Match
Best Local Similarity 53.1.
The 76; Conservative
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Best Local Similarity 53.1<sup>†</sup>
Matches 76; Conservative
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CORRESPONDENCE ADDRESS:
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APPLICANT: Sim, K
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ORGANISM: Pla
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US-08-568-459A-1
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450 TGCCATATCAACACAGTCCCTTTCCTATACATCGGCAGCTCATTATTATAGTTGATGTTG 509
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                                                                                                                                                                                                                      Score 35.6; DB 2; Length 4:
Pred. No. 0.048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    510 AATTCAGAAAACAAAATCTCATTCTTGTCTGCTGNAAGAGTTC 552
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Pred. No. 0.043;
94; Mismatches 120;
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OTHER INFORMATION: n = A,T,C or G
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.9%;
Matches 83; Conservative
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Best Local Similarity 7.8%;
Matches 18; Conservative 9
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                                                                                                        LENGTH: 451 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                  TELEFAX: 206-442-6678
                                                                                                                                                                                     MOLECULE TYPE: Other
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LOCATION: (1)...(289)
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                                                                                                                         Parent No. 5198347

APPLICANT: Miller, LOUIS H.; ADAMS, JOHN H.; KASLOW,
DAVIC C.; FANG, XIANGDOUG

TILLE OF INVENTION: DNA ENCODING PLASMODIUM VIVAX AND
PLASMODIUM KNOWLESI DUFFY RECEPTOR
NUMBER OF SEQUENCES: 27

CURRENT APPLICATION DATA:

PELLING DATE: 20-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                       Score 35.8; DB
Pred. No. 0.15;
0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: LUNN, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
                                1496 ATTTACAAATCCATATAAAATTC 1474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1496 ATTTACAAATCCATATAAAATTC 1474
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APPLICATION NUMBER: US/08/943,087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08943087
Patent No. 5945511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZymoGenetics, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jelmberg, Anna C. Adams, Robyn L.
                                                                                                                                                                                                                                                                                                                                                                         6.0%;
53.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 53.1
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lok, Si
Kho, Choon J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                 LENGTH: 4084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                               SEQ ID NO:5
                                                                                          RESULT 6
5198347-5/c
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1735 CGTCATCGTCATCGTCATC 1717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       470 TTTCCTATACATCGCCAGC 488
                        ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 52.50,
Local 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2295 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                      (617)542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
    CORRESPONDENCE ADDRESS:
                                                                                                                  ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                           Fasse, J. P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA
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                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                              STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
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                                                                                                                                                                                                                                                                                                                       NAME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE PRODUCTION IN TITLE OF INVENTION: THE ABSENCE OF NONSENSE-MEDIATED MRNA DECAY FUNCTION NUMBER OF SEQUENCES: 6
478 ACATCGGCAGCTCATTATTATAGTTGATGTTGAATTCAGAAAACAAAATCTCATTCTTGT 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            418 TAATTICTITIGICATCACTICATCCACCTICTGCCATATCAACACAGGCCCTTTCCTAT 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        478 ACATCGGCAGCTCATTATTATAGTTGATGTTGAATTCAGAAAACAAAATCTCATTCTTGT 537
                                       114 NYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYCY 55
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                                                                            538 CTGCTGNAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTACTGGTGTTAGTCC 589
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                                                                                                   54 AYTYTYGYTYAYAYTYTYGYTYAYAYAYTYAYGYTYAYAYTYTYGYTYTYGYTYCYCY 3
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APPLICANT: Szostak, Richard W.
APPLICANT: Szostak, Richard W.
APPLICANT: Roberts, Richard W.
APPLICANT: Roberts, Richard W.
TITLE OF INVENTION: ELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: EUSIONS
FILE REPRENCE: 00786/350007
CURRENT APPLICATION NUMBER: 08/09/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER PELING DATE: 1997-01-06
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER PILING DATE: 1999-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 289;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.9%; Score 35.4; DB 4; 7.8%; Pred. No. 0.043; tive 94; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THER INFORMATION: Translation template
                                                                                                                                                                                                                 Sequence 17, Application US/09244796 Patent No. 6281344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)...(289)
OTHER INFORMATION: n = A,T,C or G
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Patent No. 5679566
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Feng, He APPLICANT: Jacobson, Allan S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 17
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1855 CAAGATCACCACCATACTCCAAATCAGAGTCGCTGTCTTCTTCTTCTTCATCATCATT 1796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: He, Feng
APPLICANT: Jacobson, Allan S.
TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE PRODUCTION IN THE
TITLE OF INVENTION: ABSENCE OF NONSENSE-MEDIATED MRNA DECAY FUNCTION
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,300 FILING DATE: 20-JAN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUFTWARE: FRANCES FOR WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/no/1-7-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33.4; DB Pred. No. 0.68; 0; Mismatches
Suite 3100
                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 32,983
REFRENCE/DOCKET NUMBER: 04020/046001
TELECOMMINICATION:
TELECOMMINICATION: (617)542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: Fish & Richardson P.C. 225 Franklin Street
                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Sequence 1, Application US/08375300
Sequence 1, Application US/08375300
Patent No. 5679566
Patent No. 5679566
APPLICANT: Feng, He
APPLICANT: Jacobson, Allan S.
TITLE OF INVENTION: THE ABSENCE OF NONSENSE-MEDIATED mRNA DECAY FUNCTION NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS: ADDRESSE: Fish & Richardson STREET: 225 Franklin Street Suite 3100
                                                                                                                                                                                                                                                                                                                                              1855 CAAGATCACCACATACTCCCAAATCAGAGTCGCTGTCTTCTTCTTCTTCATCATCATCAT 1796
                                                                                                                                                                                                                                                                                                                                                                                                                                   1795 CCTCATCATCATCATCTTCATCATCATCCTCATCGCCTTCTTCTCCATCATCATCATCAT 1736
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                                                                                                                                                                                                               Length 2295;
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                                                                                                                                                                                                                                                        66; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US,008/375,300
FILING DATE: 20-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                     350 CAAGGCCACTGGCTTTGTCCTGGTCCGGGTCACTGCCATC
                                                                                                                                                                                                               Score 33.4; DB 5;
Pred. No. 0.68;
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Pred. No. 0.96;
0; Mismatches 66;
                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Fasse, J. P.
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04020/046001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1735 CGTCATCGTCATCGTCATC 1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              470 TTTCCTATACATCGCCAGC 488
                                                                                                                                                                                                               Query Match
Best Local Similarity 52.5%;
Matches 73; Conservative
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Best Local Similarity 52.5%;
Matches 73; Conservative
TELEX: 200154
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 2295 base pairs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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EDNESS: single
                                                                                 nucleic acid
                                                                                                                              linear
                                                                                                                                                MOLECULE TYPE: DNA
PCT-US95-16930-3
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ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boston
                                                                                   TYPE: nuclei
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                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33.4; DB 3; Length 2295; Pred. No. 0.68; O; Mismatches 66; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HETEROLOGOUS POLYPEPTIDE
PRODUCTION IN THE ABSENCE OF
NONSENSE-MEDIATED MRNA DECAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Fish & Richardson
225 Franklin Street Suite 3100
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REFERENCE/DOCKET NUMBER: 04020/046W01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US95/16930
FILING DATE: 27-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 20-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fasse T not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application PC/TUS9516930 GENERAL INFORMATION:
                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/955,472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1735 cercarcercarcercarc 1717
                                                                   ATTORNEY AGENT INFORMATION:
NAME: FASSE, J. PETER
NAME: FASSE, J. PETER
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-5070
TELEFAX: 617/542-9806
TELEFAX: 617/542-9806
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2295 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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Best Local Similarity 52.5'
Matches 73; Conservative
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TITLE OF INVENTION: PRO
TITLE OF INVENTION: NON
TITLE OF INVENTION: FUN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear;
; MOLECULE TYPE: cDNA
US-09-177-431-3
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STREET: 222
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PCT-US95-16930-3/c
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                                      3244 CCTCATCATCATCATCATCATCATCCTCATCGCCTTCTTCTCCATCATCATCAT 3185
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410 TGGCAGCTTAATTTCTTTTGTCATCACTTCATCCACCTTCTGCCATATCAACACAGTCCC 469
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                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09177431

Patent No. 6071700
GENERAL INFORMATION:
APPLICANT: He, Feng
APPLICANT: Jacobson, Allan S.
TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE PRODUCTION IN THE
TITLE OF INVENTION: ABSENCE OF NONSENSE-MEDIATED MRNA DECAY FUNCTION
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             350 CAAGGGCACTGGCTTTGTCCTGGTCCGGGTCACTGCCATCTTTTTCCTTTCCATTTCTGT
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Pred. No. 0.96;
0; Mismatches 66; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            410 TGGCAGCTTAATTTTCTTTTGTCATCACTTCATCCACCTT
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastENG for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,431
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                                                                                                                                                              470 TTTCCTATACATCGGCAGC 488
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REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 0791
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-9806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 52.5%;
Matches 73; Conservative
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 4080 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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COUNTRY: U
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TELEX: 20
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3184 CGTCATCGTCATCGTCATC 3166

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3304 CAAGATCACCACCATACTCCCAAATCAGAGTCGCTGTCTTCTTCTTCTTCATCATCAT 3245
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Pred. No. 0.96;
0; Mismatches 66; Indels 0
                                     APPLICANT: UNIVERSITY OF MASSACHUSETTS MEDICAL SCHOOL TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE TITLE OF INVENTION: PRODUCTION IN THE ABSENCE OF TITLE OF INVENTION: NONSENSE-MEDIATED MRNA DECAY TITLE OF INVENTION: FUNCTION NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESS: Rich & Richardson STREET: 225 Franklin Street Suite 3100
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER FELDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: PCT/US95/16930
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,300
FILING DATE: 20-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: FSSSS, J. PECTE
NEGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04020/046W01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Job time : 46 secs
Sequence 1, Application PC/TUS9516930 GENERAL INFORMATION:
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Best Local Similarity 52.5%;
Matches 73; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 200154
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 4080 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                   STATE: MA
STATE: MA
COUNTRY: USA
TIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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STREET: 241
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Sequence 17, Appl Sequence 26138, A Sequence 9764, Ap

66256

Sequence 80, Appl Sequence 227, App Sequence 16, Appl

Sequence 7248, Ap Sequence 455, App Sequence 1, Appli Sequence 1, Appli Sequence 8, Appli Sequence 8, Appli

0 US-09-864-761-26138 0 US-09-864-761-9764 US-10-198-846-7248 US-10-106-698-455 US-10-156-610-1 US-09-847-946A-1 US-10-243-4968-1 US-09-844-988-8 US-10-338-462-8

Sequence 14, Appl Sequence 2713, Ap

Sequence 82, P Sequence 82, P Sequence 82, P

US-10-138-838-82 US-10-139-031-82 US-10-138-905-82

Sequence 3, Sequence 61, Sequence 82, Sequence 82,

US-10-270-333-61

ALIGNMENTS

Sequence 1,

Sequence 8, As Sequence 50, 2 Sequence 14, 2

US-09-844-908-8 US-09-771-161A-50 US-09-796-872-14 US-09-764-877-2713

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APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Zhang, Jie
APPLICANT: Chang, Jie
APPLICANT: Chang, Jie
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: NO. US200120197679Alel Nucleic Acids and
TITLE OF INVENTION: POLYPeptides
FILE REFERENCE: 784CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/098,841
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 331
SOFTWARE: PL FL Genes Version 1.0
SOFTWARE: 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 171, Application US/10098841
Publication No. US20020197679A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xu, Chongjun
Zhou, Ping
Ma, Yunding
Wang, Jian-Rui
Zhao, Qing A.
Ren, Reiyan
Chen, Rui-hong
Wang, Dunrui
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2931
19820
4145
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
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), LOCATION: (42)..(938)
US-10-098-841-171
                                                                          APPLICANT: APPLICANT:
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Sequence 10017, A
Sequence 968, App
Sequence 104, App
Sequence 104, App
Sequence 11778, A
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Sequence 11, Appli
Sequence 11, Appli
Sequence 8420, Ap
Sequence 2718, Ap
Sequence 2729, Ap
Sequence 7651, App
Sequence 7651, App
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Sequence 297, App
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8282.800 Million cell updates/sec
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1 ttggaatagttcttgcttta......ggtgttagtccagattgttg
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/PCTUB_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US00_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US00_NEW_PUB.seq:*
                                                                                                         July 12, 2003, 13:41:28 ; Search time 114 Seconds
              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-198-846-10017
US-10-106-698-968
US-10-184-644-104
US-10-184-634-104
US-10-184-634-104
US-10-9864-761-3526
US-10-106-698-3112
US-10-106-698-3112
US-10-153-273-1
US-10-153-273-1
US-10-153-273-1
US-10-173-15-10
US-10-13-15-10
US-10-13-15-10
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US-09-960-352-7651
US-09-925-301-227
US-10-125-540-194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published_Applications_NA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                          - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Sequence 194, App

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; Sequence 968, Application US/10106698; Publication No. US20030109690A1; GENERAL INFORMATION:
               = A, T, C or
                                                               99.4%;
llarity 99.7%;
Conservative
; LOCATION: 1512
; OTHER INFORMATION: n
US-10-198-846-10017
                                                               Query Match
Best Local Similarity
Matches 595; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
US-10-106-698-968/c
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                                                                                                                                                                                                                                                                                                                                                                               981 GGGCTTGCATGGTTAAGCACCACAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTA 922
                                                                                                                                                                                                                                                                                                                                                                                                                 GAATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                921 GAATCTCTGGATGTTCCTTCCAGAAGCATCCCCGATGATATCGCAGTGCAAGGGCCACTG 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTCTTTTGTCATCACTTCATCCACCTTCTGCCATATCAACACAGGTCCCTTTCCTATACA 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: X1, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MI-049
CURRENT FILING DATE: 2002-07-18
FRICA PRICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10017
                                                                                                                                                                   ACCCCCATCCCTTCCTTCCTGTTCCCTCCCTCCCAACTTGAGTTGTGTCATTCGCACC
                                                                                                                                                                                                                                                                                  AGTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGA
                                                                                                                                                                                                                                                                                                                 1041 AGTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGAGGTGGGA
                                                                                                                                                  AAGGAACCATGTTCCAACACGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACC
                                                                                                                                                                                                                                     1101 ACCCCCATCCATCCCTTCCTTCCCTGTTCCCCTCCCAACTTGAGTTGTGTCATTCGCACC
                                                Gaps
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LOCATION: 1492, 1493, 1494, 1495, 1496, 1497, 1498, 1499, 1500, 1501,
LOCATION: 1502, 1503, 1504, 1505, 1506, 1507, 1508, 1509, 1510, 1511,
                                                  ..
             Length 1231;
                                                1; Indels
               Score 597; DB 9; I
Pred. No. 8.3e-178;
0; Mismatches 1;
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Publication No. US20030099974A1
GENERAL INFORMATION:
               99.8%;
             Query Match
Best Local Similarity 99.8
Matches 597; Conservative
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ORGANISM: Homo sapiens
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GTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGAG 1247
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                                                                                                                                                                                                                                                                                                                                                                                      1246 GGCTTGCATGGTTAAGCACACAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTAG 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1186 AATCTCTGGATGTTCCTTCCAGAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTGG 1127
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                                                                                                                                         AGGAACCATGTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACCA
                                                                                                                                                                                                            122 CCCCCATCCATCCCTTCCCTGTTCCCCTCCCAACTTGAGTTGTGTCATTCGCACCA
                                                                                                                                                                                                                                    CCCCCATCCATCCCTTCCTTCCTTTCCCTCCCCCCAACTTGAGTTGTGTCATTCGCACCA
                                                                                                                                                                                                                                                                                  GTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGAG
                                                                                                                                                                                                                                                                                                                                                     GGCTTGCATGGTTAAGCACACACAGAACTGAAGCGCCAAAAGGGTCAGCTGTCTTCATCTAG
                                      Gaps
                                                                       Length 1512;
                                    Indels
Score 594.4; DB 9;
Pred. No. 6.2e-177;
0; Mismatches 2;
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US-10-184-634-104/c
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LENGTH: 750
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                                                                                                                                                 482 AGGAACCATGTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACA 423
                                                                                                                                                                                CCCCCATCCATCCTTCCTTCCCTGTTCCCCTCCCAACTTGAGTTGTGTCATTCGCACCA 181
                                                                                                                                                                                                   CCCCCATCCATCCTTCCTTCCTGTTCCCTCCCAACTTGAGTTGTGTCATTCGCACCA 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCTTTGTCATCATCATCCACCTTCTGCCATATCAACACAGTCCCTTTCCTATACAT 63
                                                            GGCTTGCATGGTTAAGCACACCAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                               CTTTGTCCTGGTCCGGGTCACTGCCTTTTTTTTCCTTCCATTTCTGTTGGCAGCTTAAT
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CURRENT APPLICATION NUMBER: US/10/184,644

CURRENT FILING DATE: 2002-06-28

Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612

SEQ ID NO 104

LENGTH: 750
                               Gaps
                               .;
0
Length 557;
                               Indels
Score 541.6; DB 9;
Pred. No. 1.6e-160;
1; Mismatches 0;
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 90.6%;
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Wood, William I.
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                               Conservative
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CORGANISM: Homo Sapien
US-10-184-644-104
              Similarity
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               Best Local Sim:
Matches 541;
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 Query Match
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132 TCCCTTCCTTCCCTGTTCCCCTCCCAACTTGAGTTGTGTCATTCGCACCAGTGTCCTGGG 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     623 MK...DMKS.SR.MHTRMY.BBTRHYGH...B.SNT...BKCCYB.TBA.DRM.K.HR.M 564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372 GTCCGGGTCACTGCCATCTTTTTCCTTCCATTTCTGTTGGCAGCTTAATTTCTTTTGTC 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 TGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGAGGCTTGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 GTTAAGCACACCAGAACTGAAGCGCAAAAAGGGTCAGCTGTCTTCATCTAGAATCTCTGGA
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P943-081/C217
CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
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Length 750
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NUMBER OF SEQ ID NOS: 612
Query Match 6.4%; Score 38; DB 9; Lø
Best Local Similarity 9.0%; Pred. No. 0.18;
Matches 39; Conservative 132; Mismatches 263;
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6.4%; Score 38; DB 9; Le
Best Local Similarity 9.0%; Pred. No. 0.18;
Matches 39; Conservative 132; Mismatches 263;
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Wood, William I.
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Gurney, Austin L.
Pan, James
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Goddard, Audrey
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica.^2.
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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SWISSRROT HIT: Q37376, EVALUE 1.40e+00
NT HIT: D13987.1, EVALUE 8.80e-01
EST_HUMAN HIT: AV693827.1, EVALUE 2.00e-12
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PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01.30
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION UNMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01.29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
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Pred. No. 0.15;
0; Mismatches 29;
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PRIOR FILLING DATE: 2000-02-04
PRIOR FILLING DATE: 2000-02-04
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-06-08
PRIOR FILLING DATE: 2000-08-03
PRIOR FILLING DATE: 2000-08-03
PRIOR PELLING DATE: 2000-10-04
PRIOR FILLING DATE: 2000-10-04
PRIOR FILLING DATE: 2000-10-07
PRIOR PILLING DATE: 2000-09-27
PRIOR PILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
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Patent No. US20020048763A1
GENERAL INFORMATION:
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65.1%;
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Best Local Similarity 65.13
Matches 54; Conservative
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LENGTH: 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431
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                                                                                                                                                                                                                                                                                                         504
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   H..C..H..TY...K..HNKKY.B..NSMH.H..Y.S.MST..A.NMBTS..SH.SBSRA 624
                                                                      192 TGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGAGGGCTTGCATG 251
                                                                                                                                                                                                                               252 GTTAAGCACACAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTAGAATCTCTGGA 311
                                                                                                                     623 MK...DMKS.SR.MHTRMY.BBTRHYGH...B.SNT...BKCCYB.TBA.DRM.K.HR.M
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING.DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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APPLICATION NUMBER: PCT/US01/00669
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APPLICATION NUMBER: PCT/US01/00667
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APPLICATION NUMBER: PCT/US01/00663
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LING DATE: 2000-05-26
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FILING DATE: 2000-08-03
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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CTHER INFORMATION: a equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (4197...(419)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (4357...(435)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (4437...(443)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (4437...(443)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (4449)
               INFORMATION: n equals a,t,g, or c
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JTHER INFORMATION: n equals a,t,g, or c
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.OCATION: (589)..(580)
THER INFO.
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LOCATION: (474)..(476)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LOCATION: (484)..(484)
                                                                                       or
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OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature LOCATION: (564)...(565)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature LOCATION: (578)
OTHER INFORMATION: n equals a,t,g, or OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature LOCATION: (581)...(581)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (449)...(449)
OTHER INFORMATION: n equals a,t,g, o
NAME/KEY: misc feature
LOCATION: (452)...(452)
OTHER INFORMATION: n equals a,t,g, o
NAME/KEY: misc feature
LOCATION: (469)...(469)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OCATION: (484)...(484)
THER INFORMATION: n equals a,t,g,
MEMEKEY: misc feature
OCATION: (491)...(491)
THER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THER INFORMATION: n equals a,t,g,
IAME/KEY: misc feature
CATION: (537). (57)
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YHER INFORMATION: n equals a,t,g,
NAME/KEY: misc_feature
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NAME/KEY: misc_feature
GOGATION: (668)...(668)...
                                                                LOCATION: (337)..(337)
OTHER INFORMATION: n equals a,t,g,
                                                                                                           NAME/KEY: misc_feature
LOCATION: (351)...(351)
UNTER INFORMATION: n equals a,t,g,
NAME/KEY: misc_feature
LOCATION: (366)...(369)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATION: (537). (537)
HER INFORMATION: n equals a,t,g,
HE/KEY: misc_feature
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THER INFORMATION: n equals a,t,g,
MEN/KEY: misc feature
OCATION: (587)..(587)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3112, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polymucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT PAPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR PILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/167,137
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ 1D NOS: 8564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             379 TCACTGCCATCTTTTTTCCTTCCATTTCTGTTGGCAGCTTAATTTCTTTTGTCATCACTT 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: MAP TO AL139805.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.6
US-09-864-761-15256
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR FILING DATE: 2001-01-30
PRIOR PAPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PELICATION NUMBER: US 60/234,687
PRIOR PPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SCD ID NO 15256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.1%; Score 36.6; DB 10; Best Local Similarity 65.1%; Pred. No. 0.43; Matches 54; Conservative 0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (252)..(252)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (295)..(295)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (313)..(315)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          368 CATTCACTTTTCAATTATCCAC 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature LOCATION: (321)..(321)
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LOCATION: (335)..(335)
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LENGTH: 734
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Su, Xin-zhaun
Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1616 Tririccarcacarrirircirricagrirriscacircigiggggaarricigacacaaar 1557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451 GCCATATCAACACAGTCCCTTTCCTATACATCGGCAGCTCATTATTATAGTTGATGTTGA 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   391 TTTTTCCTTCCATTTCTGTTGGCAGCTTAATTTCTTTTGTCATCACTTCATCCACCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/10020141
Publication No. US20030092013A1
Publication No. US20030092013A1
SABERAL INFORMATION:
APPLICANT: McCarthy, Jeanette
APPLICANT: Ableson, Allen
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
FILE REFERENCE: MMI-002
CURRENT APPLICATION UNMBER: US/10/020,141
CURRENT FILING DATE: 2001-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67; Indels
                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35.8; DE
Pred. No. 2.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/210,288
                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Plasmodium vivax SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1496 ATTTACAAATCCATATAAAATTC 1474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            511 ATTCAGAAACAAAATCTCATTC 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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STRANDEDNESS: single
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milarity 53.1%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 76; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1789 GCAAAAAAAAATGTCAAGAGTATTTATTACCGATAAATGAACATTTAACTAGCCTTTT 1848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         382 CTGCCATCTTTTTCCTTCCATTTCTGTTGGCAGCTTAATTTCTTTTGTCATCACTTCAT 441
                                                                                                                                                                                                             403 TITICIGITIGGCAGCTIAATTICITITIGICATCACTICATCCACCTICIGCCATAICAACA 462
                                                                                                                                                                                                                                                             388 TTTTTTTTGAAAAATTTTTTTTTTTTTTTAAAAAGCCCCTTTANTTTTTTTTAAAT 447
                                                                                                                                                                                                                                                                                                             463 CAGTCCCTTTCCTATACATCGGCAGCTCATTATTATTAGTTGATGTTGAATTCAGAAACA 522
                                                                                                                                                                                                                                                                                                                                                          448 ANGGNTTTTTTAAAATTGGNCCCCNNNTTTTTTANTTTAAANTTTTTAAAAAAAA 507
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) OTHER INFORRATION: Incyte ID No. US20030119009A1 1292280CB1
US-10-084-817-297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73; Indels
                                                                                                                                                              78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Susan Stuart
APPLICANT: Staten Stuart
APPLICANT: Jed G. Nuchtern
APPLICANT: Sharon E. Plon
APPLICANT: Alason M. Shohet
TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
FILE REFERENCE: PA-0046 US
CURRENT APPLICATION NUMBER: 00/270,784
PRIOR PAPLICATION NUMBER: 60/270,784
PRIOR PELLING DATE: 2001-02-25
PRIOR FILING DATE: 2001-02-25
NUMBER: OF SEQ ID NOS: 365
SOFTWARE: PERL Program
SEQ ID NO 297
                                                                                                              DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1849 IGGTATGGTAAAGAGATGTCAAAATGTGATTCT 1881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       508 AAATTTTAATTGTTTTTNNAAAAATTTNCC 539
                                                                                                                                                                                                                                                                                                                                                                                                         523 AAATCTCATTCTTGTCTGCTGNAAGAGTTCCC 554
                                                                                                              Score 36.2; DB
Pred. No. 0.65;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guery Match
6.1%; Score 36.2; DE
Best Local Similarity 52.3%; Pred. No. 1.2;
Matches 80; Conservative 0; Mismatches
Sequence 297, Application US/10084817
Publication No. US20030119009A1
GENERAL INFORMATION:
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Patent No. US20020169305A1
GENERAL INFORMATION:
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Chitnis, Chetan
Miller, Louis H.
                                                                                                           Query Match
Best Local Similarity 48.7%;
Matches 74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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331 CCCCGATGATATCGCAGTGCAAGGCACTGGCTTTGTCCTGGTCCGGGTCACTGCCATCT 390
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                    5.9%; Score 35.4; DB 9; Length 432; 43.1%; Pred. No. 0.85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.2;
63; Mismatches 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C30
    PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/123,155
CURRENT FILING DATE: 2002-04-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 10, Application US/10123155; Publication No. US20030068794A1; GENERAL INFORMATION:
                                                                                                                                                                                                                            LOCATION: (1). ... (432)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gerritsen, Mary E
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                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 43.13
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gurney, Austin L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumas, Daniel
                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                   NAME/KEY: misc feature
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Best Local Similarity
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Publication No. US20030096248A1

GENERAL INFORMATION:

APPLICANT: MCCATTHY, Jeanette

APPLICANT: Daley, George

APPLICANT: Bolk, Stacey

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE

FILE REFERENCE: MMI-003

CURRENT APPLICATION NUMBER: US/10/017,721

CURRENT FILING DATE: 2001-12-14

PRIOR PLIING DATE: 2001-12-14

PRIOR FILING DATE: 2001-004

PRIOR FILING DATE: 2001-10-17

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 185695
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                                                                                                                                                                                                                                                                                                                 42; Indels
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Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
                                                                                                                                                                                                                                                                                          Pred. No. 25;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
6.0%; Score 35.8; Di
Best Local Similarity 59.2%; Pred. No. 25;
Matches 61; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                   6.0%; Score 35.8;
59.2%; Pred. No. 25
PRIOR APPLICATION NUMBER: US 60/313,097
PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: US 60/327,485
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                        Best Local Similarity 59.2
Matches 61; Conservative
                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-10-017-721-1
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                                                                                                                                                          185695
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-10-017-721-1/c
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US-10-020-141-11
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                                                                                                                                                       LENGTH:
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APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPIJOO:
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
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                                                                                                                                                                                                          445 CCSDYYCYSYSYSYSYSYSYSYSYSYTDYCSYRRCCCYYSYSSSYSSSAST 386
116 ACACCACCACCATCCATCCCTTCCCTGTTCCCTCCCAACTTGAGTTGTGTCATTC 175
                              505 SYS.S.SWSSYSYSSSDDY.CYCCYYRYHCSDSYSYSYYY.CRCCYYT.SYSRYDCHYSC 446
                                                                                                                                                                           236 TGGGAGGGCTTGCATGGTTAAGCACACAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTC 295
                                                                                                                                                                                                                                                                    296 ATCTAGAATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGG 355
                                                                                                                                                                                                                                                                                              385 SSSSSSSYYYTSTNYC.T.CC...T..MCAABCSTTTTTTTTT..HSCC.SA..A. 326
                                                                                                                                                                                                                                                                                                                                                         325 M.YC.A.SYSYSYS.SSS.S.SYMR.HRA.SHYYTRS..S.MYCY.YM.Y..YY.YYSY 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         476 ATACATCGGCAGCTCATTATATAGTTGATGTTGAATTCAGAAAACAAAATCTCATTCTT 535
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Pred. No. 2.4;
0; Mismatches 38;
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PRIOR APPLICATION NUMBER: US 60/227,866
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PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER: OF SEQ ID NOS: 5379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2718, Application US/09938842A Patent No. US20020160378A1 GENERAL INFORMATION:
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2718
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Best Local Similarity 60.4%;
Matches 58; Conservative
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SM Homosapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

SK NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NAtional Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbe-remail.nih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40UP from Gibco

High quality sequence stop: 425.

Location/Qualifiers
AA862635 oh07e08.s
AA877204 ob09g07.s
W93044 zd93f03.s1
AU134061 AU134061
AL530910 AL530910
W93172 zd93f03.r1
BQ776022 UI-H-FH0-
BQ073764 AGENCOURT
W72675 zd68aI0.s1
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AW644038 cm36g01.w
BG018350 de67h07.y
AV718160 AV718160
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Copyright (c) 1993 - 2003
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81.2
79.3
74.6
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Score

Result No.

555 499.4 485.6 474 446 440.8

400

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/issue type="neuroblastoma cells"
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/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
8371 Email: fliang@lifetech.com URL:
http://fullength.invitrogen.com"

a 224 c 178 g 252 t 14 others
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                Chordata, Craniata, Vertebrata, Butele
Primates, Catarrhini, Hominidae, Homo.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Pred. No. 7.9e-127;
9; Mismatches 10;
                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="CSODD003XJ17"
/clone_lb="LTI_NFL001_NBC4"
/sex="male"
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Mammalia; Eutheria;
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                                 / Add. Total = "Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NDHSF pool 1: 309384-310919, 323208-328995 Soares NDHSP pool 1: 150407, 151176-152327 Soares NDEAPP pool 1: 782280-756583, 722104-774407 Soares NDHPA pool 1: 783280-750583, 722104-774407 Soares NDHPA pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."
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Homo sapiens cDNA clone CS0DD003YJ17 3
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    clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
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Pred. No. 3.7e-142;
; Mismatches 1;
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Best Local Similarity 99.8%;
Matches 555; Conservative
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bb55g04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3010614 3', mRNA sequence.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 479)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Opter_ESTs: bb55g04.y1

Other_ESTs: bb55g04.y1

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC
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JUCTALLY...

JUCTALLY...

JORGANISM="Homo sapiens"

/dD xref="taxon:9606"

/clone="IMAGE:5013768"

/clone="IMAGE:5013768"

/tissue_type="epidermoid carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: salivary gland; Vector: porB7; Site_1: Xho1;

Site_2: EcoR1; cDNA made by oligo-dT priming.

Directionally cloned into EcoR1/Xho1 sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M: Rubin

(University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                 BIO84544 881 bp mRNA linear EST 20-JUN-2001
602669101T1 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:5013768 3',
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1 (bases 1 to 881)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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TCCCTTGGGCTTGTACTGGTGTTAGTCCAGATTGTTG 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligared to an EcoR I adaptor, digested with Not I. and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are CGTC, AACG, GGGCC, GGAAG, TAGC, ATGG, ATGG, ATGGA, ATCAC. For additional information, contact: Bento Soares, bento-soares@wiewa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 01-JUN-2000 mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Corract: John Quackenbush
The Institute for Genomic Research
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IMAGE: 3104658 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Thissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov
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Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 466)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Caneer Institute, Cancer Genome Anatomy Project (CGAP),
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COMMENT

us-09-914-191-1.rst

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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
DNA Sequencing by: Washington University Genome Sequencing Clone
Clone distribution: NCI-DO Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 421.
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EST179347 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end, mRNA sequence.
AA308526
AA308526.1 GI:1960854
EST.
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                                                                                                                                                                                                                                                                                       /note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Ist etrand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatina Bonaldo.

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    Ph.D.
    cDNA Library Preparation: M. Bento Soares,
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Pred. No. 2.5e-109;
0; Mismatches 2;
                                                                                                                                                                                            /organism="Homo sapiens"
/db xref="taxon:9606"
/Clone="IMAGE:1457126"
/clone lib="NCI CGAP_Kid3"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                               577;
                                                                                                                                                                                                                                                                                         Score 440.8; DB 10; Length
Pred. No. 1.1e-110;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                      111 others
9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-Yômail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                           // 1000 sapiens"

/ organism="Homo sapiens"

/ db xref="taxon:9606"

/ clone lib="MAGE resequences, MAGC"

/ note="Vector: pBluescriptSKm"

/ note="Yector: pBluescriptSKm"
                                                                                                 Seq primer: Reverse.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                         73.78;
96.28;
                                                        Email: johnq@tigr.org
Plate: 67
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Unpublished (1997)
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AUTHORS
TITLE
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Email: cgapbs-remediatory, first.

Email: cgapbs-remediati.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NGI-GAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stops 417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA877204 1.00 432 bp mRNA linear EST 25-MAR-1998
GNAGCTTAATTTCTTTTGTCATCACTTCATCCACCTTCTGCCATATCAACACAGTCCCTT 128
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                                                                              531
                                                                                                                                                                                  TCTTGTCTGCTGNAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTACTGGTGTTAGTCCAG 591
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/clone="IMAGE:1323228"
/clone_lib="NCI_CGAP_Kid3"
/lab_host="DH108"
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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Best Local Similarity 97.4%;
Matches 407; Conservative
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                                                                    Adams, M.D. Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.M., Bult, C.J., Lee, N.H., Kikrness, E.F., Weinstock, K.G., Gocayne, J.D., White, C.J., Lee, N.H., Kikrness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G. Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Heddlom, E. Hinkle, P.S. Jr., Kelley, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Soctt, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.M., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J.; Fannon, W.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
index (http://www.tigr.org/tdb/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 412 GCAGCTTAATTTCTTTTGTCATCACTTCATCCACCTTCTGCCATATCAACACACAGTCCCTT 471
                            Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="KM12SM"
/cell_line="KM12C(HCC)metastasis into mouse (liver)"
/note="Vector: pBluescript SK-; Site_1: EcoR1; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTCGCACCAGTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGG
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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The Institute for Genomic Research
712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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/db_xref="ATCC (inhost):112370"
/db_xref="taxon:9606"
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Pred. No. 3e-105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Contact: Kerlavage, AR
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ilarity 98.8%;
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AU134061 618 bp mRNA linear EST 01-AUG-2002 AU134061 OVARCI Homo sapiens cDNA clone OVARC1001188 5', mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
I (bases 1 to 618)
Ota,T.; Nishikawa,T.; Suzuki,Y.; Ishii,S.; Saito,K.; Kawai,Y.;
Yamamoto,J.; Wakamatsu,A.; Nakamura,Y.; Nagai,T.; Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics Laboratory
Helix Research Institute
152-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
FR I human cDNA project; 5' - & 3'-end one pass sequencing: Helix
Research Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."
                                                                                                                                                                                                        GGGCTTGCATGGTTAAGCACACACCAGAAGTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTA
                                                                                                                                                                                     1 TIGGAATAGTICTIGCTITATAAAATAGTACTGCGATTAAAAAAAAAGCACTICTGCCA
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0
                                                                                                            Length 374;
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.1e-91;
.es 2; Indels
                                                                                                            DB 14;
                                                                                                                                                 0; Mismatches
                                                                                                            Score 370.8;
Pred. No. 2.1
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/db_xref="taxon:9606"
/clone="OVARC1001188"
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AU134061.1 GI:10994600
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Unpublished (2000)
                                                                                                            62.0%;
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zd93f03.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone
IMAGE:357053 3', mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 374)

Hillier,L., Clark,M., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Riffin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston The WashU-Merck EST Project

Unpublished (1995)
                                                                                                                             GTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGT-GGGA 240
76 AGGAACCATGTTCCAACACGCGCAAACAAGGTGTTTCTGCTTAAACAGAGTAAGATACACCA 135
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                                                                                                                                                                                                                                        256 GGGCTTGCATGGTTAAGCACACCAAGACTGAAGCGCAAAAGGGT-AGCTGTCTTCATCTA 314
                                                                                                                                                                                                                                                                                                                                                   136 CCCCCATCCATCCTTCCTTCCCTGTTCCCTCCCAACTTGAGTTGTGTCATTCGCACCA
                                                                                                                                                          196 GTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGGA
                                                       CCCCCATCCATCCCTTCCTTCCCTGTTCCCCTCCCAACTTGAGTTGTGTCATTCGCACCA
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sex="unknown"
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/organism="Homo sapiens"

/db_xref="GDB:1273597"

/db_xref="taxon:9606"

/clone="IMAGE:357053"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W93044
W93044.1 GI:1422215
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AL530910 I GI:12794403
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                                                                                                                                                       288
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                 TGTCTTCATCTAGAATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGT
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Genoscope - Centre National de Sequencage
BP 191 91006 FYRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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0
                                                                                          Length 618,
                                              3 others
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            /tissue_type="ovary, tumor tissue"
/note="Vector: pME18SFL3"
135 c 145 g 149 t 3
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/lab_host="DH108"
                                                                                       Ouery Match 60.9%; Score 364.4; DB 9; Best Local Similarity 98.6%; Pred. No. 1.2e-89; Matches 365; Conservative 0; Mismatches 5;
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/clone="CS0DD003YJ17"
clone lib="OVARC1"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Hammalia; Butharia; Primates; Catarrhini; Hominidae; Homo.

1. (bases, 1 to 357)

1. (bases, 1 to 357)

1. Multiman, M., Kucaba, T., Eliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rikin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

1. Unpublished (1995)

1. Unpublished (1995)

1. Contact: Wilson RK

1. Washington University School of Medicine

1. Washington Park Parkway, Box 8501, St. Louis, MO 63108

1. Fax: 314 286 1800
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by Life Technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Cer
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
8371 Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
1 206 c 239 g 220 t l others
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This clone is available royalty-free through LLNL ; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 466 Std Brror: 0.00
Seg primer: mob_REGA+ET
High quality sequence stops:
Location/qualifiers
Location/qualifiers
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                                                                                                                                                                                                                            Score 349.6; DB 9
Pred. No. 1.5e-85;
1; Mismatches 1
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99.2%;
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Best Local Similarity 99.2
Matches 360; Conservative
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us-09-914-191-1.rst

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CCAAAGGAACCATGTTCCAACACGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATAC 117
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 365)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAAAGGANCCATGTTCCAACACCGCAAACNAGGTGTTCTGCTTAAACAGAGTAACA
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UI-H-FH0-bck-l-14-0-UI.s1 NCI CGAP FH0 Homo sapiens cDNA clone
UI-H-FH0-bck-l-14-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                    2 others
                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                          /clone="IMAGE:357053"
/clone_lib="Soares_fetal_heart_NbHH19W"
/sex="unknown"
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t
                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
1. .357
/organism="Homo sapiens"
/db_xref="GDB:1273597"
/db_xref="taxon:9606"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
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BQ776022.1 GI:21984498
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98.9%;
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Matches 347; Conservative
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Unpublished (1997)
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Gaps

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237

297

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/dev stage="human chondrosarcomma ceri nine"
//dev stage="human chondrosarcomma ceri nine"
//lab_host="DH10B (Life Technologies)"
//notce="Organ: Bone; Vector: pT713-Pec (Pharmacia) with a modified polylinker; Site 1: ECOR I; Site_2: Not I;
NCI CGAP FHO is a CDNA library containing the following tissue(s): Human Grade 1 Chondrosarcomma Cell Line The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded CDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonuclectide used to prime the synthesis of first-strand cDNA contains a library is AGAATCCGGC. The sequence tag for this library is AGAATCCGGC. The cell line was provided by Drance and the (dT)la tran University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu

Seq primer: M13 FORWARD

POLYAAYES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AAGGAACCATGTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ACCCCCATCCATCCCTTCCCTGTTCCCCTCCCAACTTGAGTTGTGTCATTCGCACC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAG_LIB=UI-H-FH0
TAG_TISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1
Chondrosarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 ACCCCCATCCATCCCTTCCTTCCCTGTTCCCTCCCAACTTGAGTTGTGTCATTCGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 AGTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAAGGCAAGGAGCCCTGGGAGGTGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                    /clone="U1-H-FHO-bck-1-14-0-U1"
/clone lib="NCI CGAP FHO"
/tissue_type="Human Chondrosarcoma Cell Line"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                     1. .365
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAG_SEQ=AGAATCCGGC"
91 c 77 a
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/db_xref="taxon:05f0".
/db_xref="taxon:05f0".
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/clone="Index:5806655"
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/note="Organ: lung; Vector: poTB7; Site_1: EcoRI; Site_2:
/note="Organ: lung; Vector: poTB7; Site_1: EcoRI; Site_2:
/note="Organ: lung; Vector: poTB7; Site_1: EcoRI; Site_2:
/note="Organ: lung; Vector: poTB7; Site_2: Anote: containing the following 5' adaptor: GGCACGGAG(0). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library.

NIH MGC Library.

228 c 288 g 236 t 2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAACACAGTCCCTTTCCTATACATCGGCAGCTCATTATTATAGTTGATGTTGAATTCAGA 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           830 AAAGGGTCAGCTGTCTTCATCTAGAATCTCTGGATG-TCCTTCCAGAAAGCATCCCCGAT 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATATCGCAGTGCAAGGGCACTGGCTTTGTCCTGGTCCGGGTCACTGCCATCTTTTTTC 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 771 GATATCGCAGTGCAAGGGCACTGG-TTTGTCCTGGTCCGGGGTCACTGCCATCTTTTTTCC 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TICCATITCTGTTGGCAGCTTAATITCTTTTGTCATCACTTCATCCACCTTCTGCCATAT 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      712 TTCCATTCCGTTGGCAGCTTAATTTCTTTTGTCACTTCATCCACCTTCTGCCATAT 653
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                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2047 row: m column: 24
High quality Sequence stop: 715.
                                                                                                                                                                               NIH-MGC http://mgr.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 8.3e-80;
0; Mismatches 3; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
  BQ073764.1 GI:19902810
EST.
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Best Local Similarity 98.2
Matches 374; Conservative
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                                                                                   Homo sapiens
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Search completed: July 12, 2003, 14:23:25 Job time : 1072 secs